STIC-Biotech/ChemLib

From:

Chan, Christina

Sent: To: Subject: Wednesday, December 03, 2003 1:57 PM Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/674237

RECEIVED

PI ase rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

From:

Davis, Minh-Tam

Sent:

Wednesday, December 03, 2003 1:54 PM

To:

Chan, Christina

Subject:

Rush search request for 09/674237

Please search in commercial database, issued patent files, PGPUB and interference:

SEQ ID NO:1, 2, and 3

Thank you.
MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

Searcher:	_
Phone:	_
Location:	_
Date Picked Up:	
Date Completed:	
Searcher Prep/Review:	
Clerical:	_
Online time:	_

TYPE OF SEARCH:	
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AA Sequences:	
Structures:	_
Bibliographic:	
Litigation:	
Full text:	
Patent Family:	

VENDOR/COST (where applic.))
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DIALOG:	_
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DRLink:	_
Lexis/Nexis:	_
Sequence Sys.:	
WWW/Internet:	_
Other (specify):	_

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Vo	luntary Results Feedback Form
>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	☐ Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Con	nments:

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

BC038963 AF180522 AR175271 AF001630

AX366305 Sequence
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AK021545 Homo sapi
AF525079 Mus muscu

BC038963 Homo sapi AF180522 Homo sapi

Sequence

AF038189

AUTHORS TITLE	REFERENCE	ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	RESULT 1 AF132478
Sengar,A.S., Wang,W., Bishay,J., Cohen,S. and Egan,S.E. The EH and SH3 domain Ese proteins regulate endocytosis by linking to dynamin and Eps15	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3723)	Mus musculus	Mis miscullis (house mouse)	AF132478.1 GI:4378884	AF132478	Mus musculus Esel protein mRNA, complete cds.	AF132478 3723 bp mRNA linear ROD 09-MAR-1999	

Q Q D Q	BASE COUNT ORIGIN Query Match Best Local Si Best Local Si Matches 3641; Qy 1 A	CDS	JOURNAL MEDLINE PUBMED PUBMED REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE
61 GAAAGGGCCAAGCATACCAGCAGTTCCTTAGCCTGAAGCCGATTGCGGGATTTATTACT 120 61 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGGATTGCTCACT 120 61 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGATTTATTACT 120 61 GAAAGGGCCAAGCATGACCAGCAGTTTTTTTTCCAATCTTGGGTTACCTCAGCCTGATCTTAGCACAA 180 121 GGTGATCAAGCCGAGGAACTTTTTTTTCCAATCTTGGGTTACCTCAGCCTGTCTTAGCACAA 180 121 GGTGATCAAGCCGAGGACATGAATAACGATGGAAGGATGAATCAAGTGGAATTTTCCATA 240 181 ATATGGGCCGCTAGCCGGACATGAATAACGATGGAAGGATGAATCAAGTGGAATTTTCCATA 240 181 ATATGGGCCGTTATCAAACTGAAATAACGATGGAAGGATGATCAAGTGGAATTTTCCATA 240 241 GCCATGAAGCTTATCAAACTGAAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 300 241 GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 300 241 GCCATGAACAGCAACCTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 300 361 GCTAGCAACAGCAACCAGTGGCTATTTCCAGTGCACCACTTTGGTATAGGAGGGATT 360 361 GCTAGCATGCAACCAGTGGCTATTTCCAGTTGCACCAGCTTTTGGTATAGGAGGGATT 360 361 GCTAGCATGCAACCAGTGGCTATTTCCAGTTGCACCAGCATTTGGTATAGGAGGGATT 360 361 GCTAGCATGCAACCAGTGGCTATTTCCAGTTGCACCAGCATTTGGTATAGGAGGGATT 360 361 GCTAGCATGCAACCAGTGGCTATTTCCAGTTGCACCAGCATTTGGTATAGGAGGGATT 360 361 GCTAGCATGCACCACCACTCACAGCTGTTTCCCAGTTGCCACACTTTCCAGTTTTTTTT	/ CD_XEEL="G1:43/885" // LTABLATION_FLISLKPIAGFI] // LTABLATION_FLISLKOLENGES // LAMILIDVANGGPLPPULPPRINTEQREEGREGGGOLUTKLOKAGSSINGULSSINDLSDIDQDC // LAMILIDVANGGPLPPULPPRINTEQREEGREADALES // LESTILAMILIDVANGGPLPPULPPRINTEQREEGREADALES // LESTILAMILIDVANGGPLPPULPPRINTEQREEGREADALES // LESTILAMILIDVANGGPLPPULPPRINTEQREEGREADALES // LESTILAMILIDVANGGPLPPULPPRINTEGERERAPLES // LESTILAMILIDVANGGPLPPULPPRINTEGERERAPLES // LESTILAMILIDVANGGPLPPULPPRINTEGERERAPLES // LESTILAMILIDVANGGPLPPULPPRINTEGERERAPLES // LESTILAMILIDVANGGPLPPULPPRINTEGERERAPLES // LESTILAMILIDVANGGPLPPULPPRINTEGERERAPLERQRQI // LERCARDLES // L	, dr / dr / dr / dr / dr / dr / dr / dr	EMBO J. 18 99164083 10064583 2 (bases Sengar A.S Direct Sub Submitted Research/D University
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Submitted (02-MAR-1999) Programs in Cancer & Blood
Research/Developmental Biology, The Hospital for Sick Children,
University Avenue, Toronto, ON MSG-1X8, Canada
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1 (bases 1 to 5145)
Sengar, A.S., Wang, W., Bishay, J., Cohen, S. and Egan, S.E.
The EH and SH3 domain Ese proteins regulate endocytosis by linking to dynamin and Eps15
EMBO J. 18 (5), 1159-1171 (1999)
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                                                            AGCTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAG
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                                            AGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAG
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J. Biol. Chem. 274 (26), 18446-18454 (1999) 99303609
                                                                                                                                                                                                                                                                                                  Submitted (11-FEB-1999) Center for Basic Neuroscience and HHMI, Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75235, USA
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Direct Submission
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Mammalia; Eutheria; Rodentia;
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KQQPAAISSAPAFGIGGMAGMPPLTAVAPVPMGSIPVVGMSPPLVSŠVEQAAVPPLAN
GAPPVLQPLPAFAHPAATLFKSSSFSRSGFGSQLMTKLQKAQSFDVASAPAAAEMAVP
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IESTNKSSELR AEITHLQQQLGESQQWLGRLIFEKQILSDQLKQVQQNSLHRDSLLT
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/protein_id="AAD30271.1"
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/db_xref="taxon:10116"
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3407; Similarity GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA, 180 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCCGATAGCGGGATTTATTACT ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATC ACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCT TCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAACTATGAGTGGACACTTA GCACAATCATTTGATGTAGCCAGCGCCCCTGCAGCGGCAGAATGGGCTGTGCCTCAGTCG GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCA 660 AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG GGGGCCCCTCCTGTCATACAGCCTCTGCCTGCATTTGCTCATCCTGCAGCCACATTGCCA GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA GGAATGTCTCCGCCCTTAGTATCTTCTGTCCCTCAAGCAGCAGTGCCTCCCCTGGCTAAC GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAAC GCTGGAATGCCACCACTGACAGCTGTTGCTCCCGTGCCAATGGGCTCCATCCCAGTTGTT GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT GTCATGAAGCAGCCAGCGAGCGATCTCTAGTGCACCAGCGTTTGGTATAGGAGGGATG GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCCTCCACACTTCCCCCT GGTGATCAAGCAAGGAACTTCTTTTTCCAATCTGGGTTACCTCAGCCCGTCTTAGCACAA GAAAGAGCCAAGCATGACCAGCAGTTCCAGAGTTTGAAGCCGATATCTGGATTCATCACT ATGGCTCAGTTTCCGACACCTTTTGGTGGGAGCCTGGACATCTGGGCCATAACCGTGGAG ACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCT **AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAACTACAGAAG** TCAATCTGGAATCTTTCCGACATTGATCAAGATGGAAAGCTCACCGCAGAAGAATTCATC TCAAGACTGAAATACAGGCAGTTATTCAACAGTCACGACAAGACCATGAGTGGACACTTA Conservative .88.7**%**; 93.2**%**; Score 3229.8; Pred. No. 0; 0; Mismatches 0 232; DB 10; Indels Length 18; 4025; Gaps 360 160 120 100 880 840 820 780 600 520 420 60 760 720 700 640 580 540 460 400 340 300 280 220

2926 CCTACTGAAAGTCCTGCTAGTCTAAAGACAGTGGCTTCCCCGGCCGCCCAAGCCAGCC	오 분 왕		1861 CAGAGGTCCCTGGAGGCAGCGGCGACTGAAGCAGAAGAGCAGGAGAGAGA
66 AAG) B &		1801 GTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAG 1860
58	ු සි ර		1741 CTCCGGGAGCAGCTGGACGAGGAGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGAT 1800
2746 CCCTGGAGAGCCAAAAAAGCACACTTAAATTTTAACAAAAGTGACGTCATCACCGTT	dg VQ		1681 AGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAG 1740
55. 	Db Qy		1621 ATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCAT 1680
6 AGT	D Q		1561 GCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTT 1620
2566 GAGAAGCCAGAAACGGACAACTGGGATACGTGGGCGGCTCAGCCTTCTCTGACCGTACCT	B 68		GAATT 15
2506 CCCTCCACAACCCCCAACAACTGGGCAGACTTCAGTTCCACGTGGCCCAGCAGCTCAAAC	B 6		1441 TTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGGTGT 1500
2446 CCTGCCCCAAACTGGCTCTGCGTGAGACCCCTGCTCCTTTGCCAGTGACCTCTTCTGAG	P Q		1381 AACAAGGAGGAGGAAGGCACGTGGTCCTGAAGGCAAGGAGGAAGACTCTGGAGTTTGAG 1440
386 AAC 438 AAC	B &		AGG 138 AGG 142
2326 GGATGGCTTGGAGGAGAGCTGAAAGGGAAGACGGGATGGTTCCCTGCAAACTATGCAGAA	B 6		1261 CAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGCCGCAAAAACGGGAACTG 1320
18 CCF	da Vo	1	AGG 1
2221 GTATATTACCGAGCGCTGTACCCCTTTGAATCCAGAAGTCACGATGAGATCACCATCCAG	B 8		GCAG ACAG
2161 CCCTGGTCTACCACAGAGAAAGGCCCGCTTACCATTTCTGCACAGGGAGAGTGTAAAAGTG	8 8		GCAGGAG GCAGGAG
2101 GACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGCTAAGCTGGCCACCCAGGCA	dg Qy		AGCGGGAGAACTTCGAGCGAGGC 108 AGCGGGAGAACTTCGAGCGAGGC 112
2041 AAGAGGGAAGACAGTGTCAGGAAGAAGAGGGGGGAAGAGAGAG	dg VQ		GCAGCAG 1
1981 GAGCATGTGCAGCAGGAGGAGGAGCCACGCCCCCGGAAACCCCACGAGGAG	Db Qy		CATA 96
1921 TTAGAGAAGCAAAAGGAAGACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTG	Qу		841 CTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCT 900

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Eukaryota;
                                         2 (bases 1 to 5381)
Pucharcos, C., Fuentes, J.J., Pritchard, M. and Estivill, X.
Direct Submission
Submitted (16-DEC-1998) Medical and Molecular Genetics Center,
Cancer Research Institute, L'Hospitalet de Llo., Avia.
Castelldefels km. 2,7, Barcelona 08907, Spain
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5381)

Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcantara, S., Alrones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
                                                                                                                                                                                                                                                                                                                                        FILL4468 5381 bp mRNA linear Homo sapiens intersectin short isoform (ITSN) mRNA, AF114488
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1. .5381
/organism="Homo sapiens'
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77.7%; ilarity 86.5%; Conservative Score 2831; Di Pred. No. 0; 0; Mismatches 0; 475; Length 5381; Indels 21; W

DB 9;

GAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCCAATATCTGGATTCATTACT GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180 388 328

GGTGATCAAGCTAGAAACTTTTTTTTTTTCAATCTGGGTTACCTCAACCTGTTTTAGCACAG ATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGTGGAGTTTTCCATA 508 240 448

GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCCTCCACACTTCCCCCT GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT 360 GCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTCTGCACTTCCCCCCT 568

300

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2620 GTACCTAGTGCTGGCCAGTTACGGCAGAGATCAGCCTTTACCCCAGCCACAGCCACTGGC 2679	. ب	558 ATTGCTGAAATCACCCACTTA	~
2560 TCAAACGAGAAACGGAAACGGACAACTGGGATACGTGGGCGGCTCAGCCTTCTCTGACC 2619	ш ш	69	σ <
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2440 TCTGCCCCTGCCCCCAAACTGGCTCTGCGTGAGACCCCTGCTCCTTTGCCAGTGACCTCT 2499	QY GACTCTGGAGTTT 1437 Db GACTTTGGAATTT 1708	1378 AGGAACAAGGAGCAGGAGGACGCCTGGACTTT	0 <
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GAGTTAGAGAAGCAAAAGGAACACGTCAGAGACGAGCTGAGGAAAGGAAAGGAAAGGAAAGGAATGG	900	841 CTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCT	σ •
B AGCRAAGGTCCCTGGAGGCAGCGCGACTGAAGCAGAAGAGCAGGAGGAGGAAGAAGCCTG	1108	781 TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATC	0 <
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8 CTTATTCCAGAGAACKGATACTCAGTGACCAGTTAAACAAGTCCAGCAGAACAGTTTG 	868	541 AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG	0 4
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Castelldefels km. 2,7, Barcelona 08907, Spain
Location/Qualifiers
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Pucharcos, C., Fuente
Direct Submission
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Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcant Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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2095 ATGCAAGACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGCTAAGCTGGCCACC 2154	2035 AGACTGAAGAGGGAAGACAGTGTCAGAAGAAGAAGGAGGCGGAAGAGCCGAAG 2094	249	1918 GAGTTAGAUAAGCAAAAGCAACGCACAGACGCAGTTCAGGAAAGGCACAAGCAATGG 1977	1858 AAGCAGAGGTCCCTGGAGGCAGCGGACTGAAGCAGAAGAGAGAG	1736 GATGITITCAACAACCAGCIGAAGGAACIGGAGGAGTIACATIGCAAACAGCAGCICCAG 1857	1738 CAGCTCCGGGAGCACGTGAACGAGGTGAACACCAGGTCAAAGCTGCAGGAGATT 1797	1678 CATAGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAGGAACTGGCCCGGCAG 1737	1818 CTTATTCCAGAAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTG 1677	1558 ATTUCTIGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGA 1617	1498 IGTICANCICAGACCCAGAGGCAAGAATICAGAGCAGGAGCAAGAAGTCIAGAGAGCTAAGA 1557	1438 GAGTTAGAAGCICTGAATGACAAAAAGCATCAGGAAAACTTCAGGATATCAGG 1497	15'8 AGGANCANGAGUCAGGAGGCACCGIGGICCTGAAGGGAGGAGGAGGACGCCTCTGGAGGTTT 143'/	1318 CTGAAAGGCAGCAACTTGAATGGAACCGAAGCGGAACTGCATCAATCA	1238 CUSUMANCUMANANGANGANGANTICAGRAGUCGCAGAGUCGCAAAA(CUGGAA 1317	1139 CASSANGS-CHANGCHGCHGGAGCHGGAGGAGCCAGCGGAGGAGCAGCGGAGCHGAGAGCAGCGGAGCHGAGCAGCGGAGCHGAGAGCAGCGGAGCHAGAGAGCAGCGGAGCAGAAGCAACTGGAACTGGAAAAGCAACTGGAAAAGCAACTGGAAAAGCAACTGGAAAAGCAACTGGAAAAGCAACTGGAAAAGCAGCGGGAGCTAGAA 1528	1108 CACCACACACACACACACACACACACACACACACACA		1289 CAATTAGAAAAGAAATTACCTGTAACGTTTGAAGATAAGAAGCGGGGAGAACTTTGAACGT 1348

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Guipponi,M., Scott,H.S., Chen,H., Sche Antonarakis,S.E.
Two isoforms of a human intersectin (1 brain-specific alternative splicing in Genomics 53 (3), 369-376 (1998)
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Guipponi, M., Scott, H.S.,
Antonarakis, S.E.
Direct Submission
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Homo sapiens intersectin
AF064243
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M., Scott, H.S.,
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chromosome="21"
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Pred. No. 0; 0; Mismatches 477; I	RNPFFQGGLPQPVLA KQQPVAISSAPPRGM GAPPVIQPLPAFARIP GSREKKYPG_TENSHD EFFILAMHIJDVAMS LEDEQQOLEKKLPVT RKERERQEGERKRQL RNRRQELLMQRNKGQ EIESTNKSRELRIAG RIKRALEAKELARQH MEBERLKKXCEGERKI KREESVKKXCGERKI KREESTALARQH MFTSTNMERFETDNMD GLQAQALYPWRAKXD IRKSTSNDSGSSES VTKKCGOMWTGTVGD GPEQLITLAPGQLIII EPKSTALAAVCQVI PSNYVKLTTDMDPSQ IBC_feature 167 406 /note="encodes 160_feature 2324 . 2524 /note="encodes 180_feature 326 /note="encodes 180_feature 310 3286 /note="encodes 110 3286 /note="encodes 110 3286 /note="encodes 110 359 3748 /note="encodes 150_feature 336 350. /note="encodes 150_feature 336. /note="enco
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1127 CAATTAGAAÁGÄATTACCTGTAACGTTTGAAGATAAAAGCGGAGAACTTTGAACGT 1186 1078 GGCAGTGTGGAGCTGGAGAGCGCCCCCCCCAGCGCCTCTTGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	481 GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCCTTGCGTTTTGCGCATCCTGCAGCCATTGCCA

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RESULT 7	Db 3767 TGA 3769	Qy 3640 TGA 3642	Oy 3580 GTTGGGCTCTTCCCATCCAATTATGTAAAGCTGACCACAGACATGGACCCCAGCCAG	3647 ATCATCAACGTCCTCAACAAGGAGGACCCTGACTGGTGGAAAGGAGAAGTCAATGGACAA	3500 ATCARGA NGCTCCTCA ACA NGCAGA CGGGGA CGGGGA AGGGAGA AGGAGA AGGGGGAA AGGGGCAA	3450 ATCCCCATCATCATCCCACCACCACCACCACCACCACCAC	340 3467	3280 ATTCTGATCCGGAAAAGAACCCAGGTGGATGGGAAGGAAG	3220 GITATIGCTICCIAGUCIGCIACIGGICCCGAGCAGCICACICCICGCCCCTGGICAGCIG 3347 GITATIGCCTCATACACCGCCACCGGCCCCGAGCAGCTCACTCTCGCCCCTGGICAGCIG	3160 GAGGGCTCTGGAACTGCTGGGAAAACAGGGAGTTTAGGAAAAAACCTGAAATTGCCCAG	3100 GAMALGGIUGGCCGACANGICCUGGAGICIIICIACALIAIGIGAGGCIIANGGCIIANGGCIICAGGCIIANGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCIIANGGCCCIIANGGCCCIIANGGCCCIIANGGCCCIIANGGCCCCIIANGGCCCCIIANGGCCCIIANGGCCCCCIIANGCCCCCCCCCC	3040 THACCTITICAGCAAGGGATGTGATTTGTGGTTACCAAGAAAGATGGTGACTGGTGACA	2980 GCATTCCCGGAGAAGAGTTATTGCCATGTACAACTACGAGGTTCTGAGCAAGGAGAT	2920 ACIGGECTACTGAAAGTCCTGCTTAGTCTAAAAGAGTGGCTTCCCCGGCCGCCAAGCCG	2860 TICCCCAAGICTIAAGITGAAACICATICAAGICCCGIFAAGAATICCACAGAGCAICGAT	2800 ACCGTTCTGGAACAGCAAGACATGTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTTGG	2/10 TIGLALIC IGGAGAGC CAAMAMACACACTIAMAIII IAACAAMAGGAACGCTTACICACCACTIAMAIII IAACAAAAATGATGATGATCATCATCATCATCATCATCATCATCATCATCATCATCA	2007 TCCTCCCCTTCCCCCCTAGGCCAGGGTGAAAAGGTGGAGGGGCTACAAGCTCAAGCC 2807 TCCTCCCCGTCCTCGTGCTAGGCCAGGGTGAAAAGGTGGAGGGGCTACAAGCTCAAGCC	2747

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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 7247)
Guipponi, M., Scott, H.S., Chen, H., Schebesta, A., Rossier, C. and Antonarakis, S.E.
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Homo sapiens intersectin long
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Direct Submission
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IRKSTSMDSGSSESPASLKRVASPAAKPVVSGEEFIAMYTYESSEQGDLTFQQGDUTL
VTKXDGDWWTGTVGDKAGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYTAT
                                                                                                                          PLGSSGTDKVFSPKSNLQYKMYKTPIFLNEVLVKLPTDPSGDEPIFHISHIDRVYTLR
AESINERTAMVQKIKAASELYIETEKKKREKAYLVRSQRATGIGRLMVNVVEGIELKP
CRSHGKSNPYCEVTMGSQCHITKTIQDTLNPKMNSNCQFFIRDLEQEVLCITVFERDQ
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EEFILAMHLIDVAMSGQPLPPVLPPEYIPPSFRRVRSGSGISVISSTSVDQRLPEEPV
    /note="encodes
2324. .2524
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/product="intersectin long
/protein_id="AAC78611.1"
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/mol_type="mRNA"
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J. Biol.
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                                                                    Okamoto,M., Schoch,S. and Sudhof,T.C. EHSH1/intersectin, a protein that contains binds to dynamin and SNAP-25. A protein cor
                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
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J. Biol. Chem. 274 (26), 18446-18454 (1999)
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Okamoto,M., Schoch,S. and Sudhof,T.C.
Direct Submission
Submitted (02-MAR-1999) Center for Basic Neuroscience
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386 AAGATTCCAGAAAATGAGGTTCCCACTCCAGCCAAACCAGTGACCGATCTGACCTTGACAICTGCC	380 420	1321 GARAGGCAGCGACAACTTGAATGGGAACGGAGACAGGAACTCCTGAATCAGAGG 1
26 GGATGGCTTGGAGGAGACCTGAAAGGAAGACGGGATGGTTCCCTGCAAACTATGCAGAA 	1320 Db 1360	1261 CAGCGAGAGGAGGAGGAGGAGGAGGATCGAGAGGCGGAGGCCGCAAAACGGGAACTG 1
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621 ATTCCAGAGAACKGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCAT	40	541 AAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG 6
561 GC156AA1CACCCACTTACAGCAGCAGTIGCAGGAATCTCAGCAAATGCTIGGAAGACTT 601 GCGGAAATCACCCACTTACAGCAACAGTTGCAGGAATCTCAGCAGATGCTTGGAAGACTT	540 Db	481 GGGGCTCCTGCCGTCATACAGCCTCTGCCGTTTTGCGCATCCTGCAGCCACATGGCCA 5
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- 1	3586 CTCTTCCCAATCAATTATGTAAAGCTGACCACAGACATGGACCCCCAGCCAATGA 3642	Ş
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	3166 TCTGGAACTGCTGGGAAAACAGGGAGTTTAGGAAAAAAAA	Ş
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TITLE Direct	2918 AAGTCTTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGC 2977	D
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MEDLINE 990304	2858 CTGGAACAGCAAGACATGTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTT	DЬ
	2806 CTGGAACAGCAAGACATGTGGTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTT	Ş
RS CE	2746 CCCTGGAGAGCCAAAAAAGACAACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTT 2805	Db Qy
Eukary Amphib	2738 CCTTCTCCCGTCCTGGGCCAGGGTGAAAAGGTGGAAGGGCTCCAAGCACAAGCCCTGTAT 2797	뮍
ORGANISM Xenopu	2686 CCATCTCCCGTCCTGGGCCAGGGTGAAAAGGTGGAAGGGCTACAAGCGCAAGCCCTGTAT 2745	8
	2678 AGTGCTGGCCAGTTAAGGCAGAGGTCGGCCTTCACACCAGCCACAGCCACTGGCTCCTCC 2737	망
DEFINITION Xenopul ACCESSION AF0321:	2626 AGTGCTGGCCAGTTACGGCAGAGATCAGCCTTTACCCCAGCCACAGCCACTGGCTCCTCC 2685	ş
	2618 GAGAAACCAGAAACGGACAACTGGGACACGTGGGCGGCTCAGCCTTCTCTGACTGTACCC 2677	뮹

RESULT 9 AF032118

misc_feature

3148. .3324 /note="encodes SH3C domain"

note="encodes SH3B domain"

2881. .3057

note="encodes

SH3A

note="encodes EHb domain" 2386. .2571

/note="encodes 850. .1101

EHa domain"

253.

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(bases 1 to 4103)
bhai, M., Hoffman, N.G., Hardison, N.L., McPherson, P.S.,
agnoli, L., Cesareni, G. and Kay, B.K.
arsectin, a novel adaptor protein with two Eps15 homology and
scre homology 3 domains
scr homology 3 domains
chem. 273 (47), 31401-31407 (1998)
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rersity Ave, Madison, WI 53706-1532, USA
Location/Qualifiers
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man, N.G., Hardis
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2118
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ibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                      ERERODQERKKQQDLEKQLEKORELEROREEERRKEIERREAAKRELERORQLEWERN
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KRALETKEIGRQLEROLDEVEKETRAKLQEIDVFNNQLKELRELYNKQQFQKQOPE
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/cell type="occyte"
193. _4005
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/note="EH domain and SH3 domain containing protein;
similar to intersectin binding proteins Ibpl, encoded GenBank Accession Number AF057285, and Ibp2, encoded b GenBank Accession Number AF057286, and mouse
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SSRLKYRQLFNSQDKTMSGNLTGPQARTILMQSSLPQSQLATIWNLSDIDQDGKLTAE
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MNVKYINI"
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1975 TGGCTGSAGCATGTCAGCAGGAGGAGCAGGCACGCCCCGGAAACCCCACGAGGAG	B &	895 CTGCCTCCAGAATACATCCCTCCTTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGATGTCC 954	. 8
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	S B 8	775 CTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAA 834 	B 8
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	D &	/ 655 CAGTCATCAAGGCTGAAATACAGGCAGGTATTCAACAGCCACGACAAAACTATGAGTGGA 714	B 8
	5 B 8	/ 595 CAGAAGGCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCT 654	B 8
615 MARCITATIC CASAGARACASATACICAS ISACCASTANACANSICCASCASARACAS) B (9	7 535 TGGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTA 594	유 성
1555 AGAATTGCTGAAATCACCCACTTACAGCAGGAGTTGCAGGAATCTCAGCAAATCTCAGCAAATCTCAGCAAATCTCAGCAAATCTCAGCAAATCTCAGCAAATCTCAGCAAGATCACAACATTGCAGCAGCAGCAGCTTCAAGAATCTCAGCAAGCTGCTTGGA 1803	Ag dg	475 GCTAACGGGGCTCCTCCCGTCATACAGCCTCTGCCTTTGCGCATCCTGCAGCCACA 534	B &
	D &	415 GTIGITGGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGCAGCCCCTCG 474	B &
	S B 8	7 355 GGATTGCTAGCATGCCACCACTGACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCA 414	B 8
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	OV DB	7 241 GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 300	음 성
	Qy Db	181 373	음 <i>성</i>
	Oy Db	121 GGTGATCAAGCGAGGACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 1	B 3
	Оу	7 61 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT 120	유 성
11)3 CAGGAGCGGTTGGCTCAGCTGGAGCGCGCCGAGGCAGGAAGAAGAGGCGGGAAGCGCCAG 1194	o p &	1 ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG 60	유 성
1015 CAGCAGCAAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAACTTCGAG 1074	\$ B &	Query Match 55.7%; Score 2027.6; DB 5; Length 4103; Best Local Similarity 73.6%; Pred. No. 0; Matches 2685; Conservative 4; Mismatches 918; Indels 39; Gaps 7;	
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                                                                                                           HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2599
PN JP 2002017375-A/2599
PN 22-JAN-2002
PT 705H10 OTA, TETSUO NISHIKAMA, TAKAO ISOGAI, KOJI HAYASHI, SHIZU PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC 12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
                                                                10,
PC C12
Primer
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2131)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer for synthesizing
BD127168
BD127168.1 GI:23222113
JP 2002017375-A/2599.
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OY 361 GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT 420	Qy 301 GTCATGAAACAGCAACCAGTGGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT 360	QY 241 GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 300	OY 181 ATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATCAAGTGGAATTTTCCATA 240	OY 121 GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180	QY 61 GAAAGGGCCAAGCATGACCAGGCAGTTCCTTAAGCCTGAAGCCGATAGCGGGATTTATTACT 120	QY 1 ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG 60	Query Match 40.7%; Score 1483.8; DB 9; Length 2131; Best Local Similarity 86.0%; Pred. No. 0; Matches 1657; Conservative 0; Mismatches 267; Indels 3; Gaps 1;	/dev_stage="embryo, 10 weeks" /note="cloning vector: pMS18SFL3" BASE COUNT 694 a 469 c 526 g 442 t ORIGIN	/db_xref="taxon:9606" /clone="HEMBA1004110" /tissue_type="whole embryo, mainly head" /clone lb="HEMBA1"	rce	Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.). FEATURES Location/Oualifiers	(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction:	JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan	NEDO huma Unpublish 2 (bases	Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Isoqai,T., Ota,T., Nishikawa,T., Havashi,K., Otsuki,T.,	AK074554. oligo cap Homo sapi M Homo sapi	DEFINITION Homo sapiens cDNA FLJ90073 fis, clone HEMBA1004110, highly similar to Homo sapiens intersectin short form mRNA. ACCESSION AK074554
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2N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/0 C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/0 rimer for synthesizing full-length cDNA and use thereof FH Location/Qualifiers CDS Location/Qualifiers 1. 2131 /organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606" 691 a 448 c 572 g 420 t	75 75 H M •	thereof. thereof. thereof.	Qy 1738 CAGCTCCGGGAGCAGCTGGACGAGGTGGAGAGACCAGGTCAAAGCTGCAGGAGATT	1618 CTTATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTG	Db 1645 GAATTAGAAGCTCTAAATGATAAAAGCATCAACTAGAAGGGAAACTTCAAGATATCAGA Qy 1498 TGTCGACTGGCAACCCAGAGGCAAGAATTTGAGAGCACGAACAAGTCTAGAGAGCTAAGA
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841 CTAGCTATGGACTTAGTGATGATGATGCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCT	Qy 601 GCACAATCATTCGATGTCGCCAGCGCCCTCCAGCAGCAGAATGGGCTGAGTCA 660	Qy 361 GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT 420 Db 692	181 527 241 587 301	61 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGGATAGCGGGATTATTACT	ORIGIN Query Match Query Match B1.2%; Score 1259.2; DB 6; Length 2131; Best Local Similarity 81.2%; Pred. No. 9.1e-275; Best Local Similarity 81.2%; Pred. No. 9.1e-275; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 114; Gaps 2; Matches 1539; Conservative 0; Mismatches 243; Indels 243; Indels

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AK027846
Homo sapiens cDNA FLJ14940 fis, clone PLACE1010942, highly to Homo sapiens intersectin long isoform (ITSN) mRNA.

AK027846
AK027846.1 GI:14042823
Oligo capping; fis (full insert sequence).

Homo sapiens (human)
Homo sapiens
    Eukaryota; Metazoa; Chordata;
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  Craniata; Vertebrata;
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  Euteleostomi;
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highly similar
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Isogai,T. and Otsuki,T.
Direct Submission
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GGGGCTCCCCCTGTTATACAACCTCTGCCTGCATTTGCTCATCCTGCAGCCACATTGCCA
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                                                                                                           GAATTAGAAGCTCTAAATGATAAAAAGCATCAACTAGAAGGGAAACTTCAAGATATCAGA
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                                                                                                                                                                                                                                                                                     AGGAACAAGGAGGAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAAGACTCTGGAGTTT 1437
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Matches 1227; Conserv
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                                                                                                                                                                                                                                                                                                    source
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HELLX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/3071
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PF TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI H
PI ISHII, AMAAI, AI WAKAMATSU, TOMOYASU SUGIYAWA, KEIIC SINIICHI KOJIWA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC TETSUJI OTSUKI, HISASHI KOGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1676)

Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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JP 2002017375-A/3071.
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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RS Isogai, T. and Otsuki, T.

Direct Submission

AL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; CDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK075290.1 GI:22761283 oligo capping; fis (full insert Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="Y79AA1000778"
/cell_line="Y79"
/cell_type="retinoblastoma"
/clone_lib="Y79AA1"
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1020 1283	961 AGCTCTTCTGTGGATCAGAGGCTGCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAG	
960 1223	01 CCAGAATACATCCCTCCTTCCGTCAGAAGAGTTCGCTCCGGCAGTGGGATGTCCGTCATA	
900	CATGTCTGGTCAGCCACTGCCGTCCTGCCT	
840 1103	1 TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATC	
780 1043	721 ACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCT	
720 983	PAACAGCCACGACAAAACTATGAGTGGACACTTA 	
660 923	01 GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGCTGTGCCTCAGTCA	
600 863	1 AAGAGTTCTTCCGTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG	
540 803	81 GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCCTTTTGCGGCATCCTGCAGCCACATGGCCA	
480 743	TTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAAC	
420 683	361 GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTT	
360 623	301 GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT	
300 563	241 GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT	
240 503	GATGGATCAAGTGGAATTTTCCATA AATGGATCAAGTGGAGTTTTCCATA	
180 443	ITTTTTTTCCAATCIGGGTTACCTCAGCCIGTCTTAGCACAA 	
120 383	TTAGCCTGAAGCCGATAGCGGGATTTATTACT	

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1378 AGGAACAAGGAGCAGGACCGTGGTCCTG 1410	1584 CTTGAAAGGCAACGACAACTTGAGTGGGAACGGAATCGAAGGCAAGAACTACTAAATCAA 1643	1318 CTGGAAAGGCAGCGACACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTGAATCAG 1377	1524 CGGCAGAGAGAGGAGGAGGAAGAAGTTGAGAGGCGAGAGGCTGCAAAACGGGAA 1583	1258 CGGCAGCGAGAGGAGGAGGAGGAGGAGGATCGAGAGGCGCGAGAGGCCGCAAAACGGGAA 1317	1464 CAAGAGCGCAAAAGACAACTGGAACTGGAAAACTGGAAAAGCAGCGGGAGCTAGAA 1523	1198 CAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAG 1257	1404 GAGCGCCTGGCCCAGCTGGAGCGGGGGGGGAGAGGAGAG

Search completed: December 4, 2003, 21:34:19 Job time : 8623.82 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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16717.740 Million cell updates/sec
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Human SH3D1A cDNA Human SH3D1A cDNA. encoding novel

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								<pre>vesicular trafficking; n; cancer; infection; docytosis; anticancer;</pre>						Mouse secreted exp	DNA encoding novel	ä	Human SH3P18 gene.	cDNA encoding nove	Human Cione 65 gen DNA encoding novel	Human polynucleoti	Human cDNA clone (DNA encoding novel	Human polynucleoti	Human ovarian carc	Human adipocyte Se	Human cDNA 5'-end	Mouse Ese2 coding DNA encoding molec	Mouse Ese2L coding	Mouse Ese2 full le	Allergic disease e Human polynucleoti	Human SH3P17 gene.	an cDNA, SEQ I	DNA encoding novel	Human cDNA sequenc	Human SH3DlA cDNA	DNA encoding novel	Human polynucleoti

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutants); (I) specific antibodies (Ab); sequences antisense to the (I) polynucleotide; agents that downregulate expression of Ese genes or antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant) agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding dynamin to the complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex with Espl5 protein), vesicular trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, mimetics, fragments and inactive
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   CCCTCCACACTTCCCCCTGTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCA
                                    CAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTC
                                                      CAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTC
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                                              GGAATATCTTGAACAAGTAATCTTCTTGACAAGAAAGAATGTATAGAAGTCTCCCTGCAA
                                                                          GGAATATCTTGAACAAGTAATCTTCTTGACAAGAAAGAATGTATAGAAGTCTCCCTGCAA
                                                                                                                                            ATCATCAGTACCCACCGTCTTAGTCTCTGTTACGTGAAGTTTATTCCAGTTGCTTTTTAT
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New nucleic acid encoding Esel and 2 proteins, for treating cancer or involved in regulation or preventing viral

WPI; 2000-052802/04. P-PSDB; AAY57449.

Claim 6; Page 56-59; 99pp; English

The present invention specifically describes mammalian Esel and 2 CC proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocytosis). (I) are involved in regulation of clathrin-CC mediated endocytosis (as a complex with Espl5 protein), vesicular CC trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, CC mimetics, fragments and inactive mutants); (I) specific antibodies (Ab); Sequences antisense to the (I) polymucleotide; agents that downregulate CC expression of Ese genes or antagonists of an Ese binding partner are CC used to treat diseases associated with undesirable endocytosis and CC resulting changes in cellular function. Particularly overexpression of CC Esel is used to block clathrin-mediated endocytosis in vivo or in cell CC cultures, while administration of (I) is used to promote endocytosis of CC selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal CC proliferation of cells that can be stimulated to proliferate by a growth CC factor receptor; and similar compounds (also inactive Ese mutants) can be CC used to prevent viral infection. Endocytosis may also be regulated, in CC vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding CC dynamin to the complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal ccc present sequence represents mouse Esell cDNA sequence.

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QY dd	DP GA	Db Qy	Qy db	B &	D Qy	Qy Db	D Q	Db 99	B 8	95 54	db Qy	Qу	B 8	D 49) B Q	B 9	Query Best Match	SQ Se
960 AACTATGAGTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTT 1019 	900 ATGGGCTGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAA 959	840 AAACACTAAGTTACAGAAGCACAATCATTCGATGTCGCCAGCCCCCCCC	780 TCCTGCAGCCACATGGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATT 839	720 AGTGCCTCCCCTGGCTAACGGGGCTCCTCCCGTCATACAGCCTCTGCCTGC	660 GGGCTCCATTCCAGTTGTTGGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGC 719	600 ATTTGGTATAGGAGGGATTGCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAAT 659	540 CCCCTCCACACTTCCCCCTGTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGC 599	480 TCAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCT 539	420 TCAGCCTGTCTTAGCACAAATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATGGA 479	360 GATAGCGGGATTTATTACTGGTGATCAAGCGAGGAACTTTTTTTT	300 CTGGGCCATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCC 359 	240 AGGTGAACGTAATAGAACCATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGT 299	180 CACTGATTTGTGTGAGGGGCGGCCGCGCGCCCCGGAGATGAGGCGTCGATCAGCA 239	120 GCGGCGGGARTGGTGTCGCGGCTGCGGACTCCGCGTTCCTCGCGCGGCGGCGGGCTG 179	60 GGCGGCTCGCAAGGGAGCATCCCGAGCGGGCTCCGGGACGGCCGGGAGGCAGGC	1 CGGCACGAGGAGGAGGAGGCGGCGC-GGGAGGGCGCAGCTTGGTTGCTCCGTAGTAC 59	rry Match 76.4%; Score 3886.4; DB 21; Length 5738; It Local Similarity 99.9%; Pred. No. 0; Indels 1; Gaps 1; Ches 3898; Conservative 0; Mismatches 1; Indels 1; Gaps 1;	equence 5738 BP; 1556 A; 1456 C; 1613 G; 1113 T; 0 other;
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, Db 49) B &	B 8	S & &	B &	}	g 42	Db Q	ρ δ	D 5) B &	₽ &	, p. 5	₽ \$	₽ ₽	\$ B \$	\$ B :	o p	8
2040 AAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTGAAGGAACTGAGGAGAGATACAT 	1980 GAGCTIGGCCCGGCAGCAGCTCCGGGAGCAGCTTGGACGAGGTGGAGAGAGA	1970 CCASCASSACASTITISCATASASSACTOSCTTCTTACCCTCAAAAGSACCCTTGGAAGCAAA 1979 2	1860 GCAGATGCTTGGAAGACTTATTCCAGAGAACXAGTACTCAGTGACCAGTTAAAACXAGT 1919	1800 GICHAGRARGUNAGAATITGCIGAAATCACCCACTIACAGCAGCAGCAGTIGCAGGAATCICA	1740 ACTTCAGGATATCAGGTGTCGACTGGCAACCCAGAGAAATTGAGAGCACGAACAA 1					1440 GCGGGAGCGCCAGGAGCAGAGGCCCAACCGGCAGCTGGAGAACAGCAGCTGGAGAACAGCAGCTGGAGAACAGCAGCTGGAGAACAGCAGCTGGAGAACAGCAGCTGGAGAACAGCAGCTGGAGAACAAGCTGGAAGCAGCTGGAGAACAGCTGGAGAACAGCTGGAGAACAGCTGGAAGAACAGAACAGAACAGAAACAGAAAAAAAA	1380 GEAGCGCAAGAGCAGGACGGTTGGCTCGAGCTGGAGCGCCGAGCAGGAGGAAGAAAGA	1320 GAGAACTTCGAGCAGGCAGTGTGGAGCAGGCCGCCAAGCGCTCTTGGAGCA			1200 CAGTGGGATGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGAGAGCCGTC			1020 ACCCCAGGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAC

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AAZ39009 standard;

CDNA;

3723 ВP

28-FEB-2000 (first entry)

Mouse Esel coding sequence

Mouse; murine; Ese1; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss.

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WO9955728-A2

04-NOV-1999

27-APR-1999; 99WO-CA00375

27-APR-1998; 05-FEB-1999; 98CA-2230201. 99US-0118739.

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mutants); (i) specific antibodies (Ab); sequences antisense to the (I) CC polynucleotide; agents that downregulate expression of Ese genes or CC antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block function. Particularly overexpression of Esel is used to block collathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. CC (Ant) agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal cell division or migration; viral infection; or abnormal cell contents is generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal cell division or migratical cell division or migration; viral infection; or abnormal cell division or migration; viral infection; or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 3723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their spli variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a compl with Espl5 protein), vesicular trafficking and actin cytoskeleton.

Generally (I) (or its (ant) agonists, mimetics, fragments and inactive denerally (I) (or its (ant) agonists (Ab); sequences antisense to the (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3723 BP; 1065 A; 941 C; 1025 G; 692 T; 0 other;
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3919. CCCCCTCAGGCTTGAAAGTCCTCAAAGAGACCCACTATCCCCATATCACTGCCCAGAGGGA 3978	2898 Qy 2640 Db		ਲੋਂ ਵੇਂ
TATGTAAAGCTGACCACAGACATGGACCCCAGCCAGCAATGAATCATATGTTGTCCATCC	2838 Db	2779 AACAACTGGGCAGACTTCAGTTCCACGTGGCCCAGCAGCTCAAACGAGAAGCCAGAAAACG :	ु र
TAMESTIC CONTINUES OF THE CONTINUES OF	2778 Db 2520 C:	2719 GCTCTGCGTGAGACCCCTGCTCCTTTGCCAGTGACCTCTTCTGAGCCCTCCACAACCCCC :	ुं र
GCCCAGAACGATGACGAACTAGCCTTCAGCAAAGGCCAGATCATCATCGTCCTCAACAAG 	2718 Db 2460 C:	2659 GAGGTTCCCACTCCAGCCAAACCAGTGACCGATCTGACATCTGCCCCTGCCCCCAAACTG :	ुं र
CONTROL OF THE CONTRO	2658 Db 2400 C	2599 GAGCTGAAAGGGAAGACGGGATGGTTCCCTGCAAACTATGCAGAAAAGATTCCAGAAAAA :	ਰ ₹
619 TTTCCAGCAAATTATGTCAAACTTCTAAGCCCCGGGAACAAGCAAATTCACCCCAACTGAG	2598 Photographic Control Cont	2539 CCAGGAGATATAGTCATGGTGGATGAAAGCCAGACTGGAAGAGCCAGGATGGCTTGGAGGA :	ਰ ੨
CCAGGTGGATGGTGGGAGGGAGAACTGCAAGGTCGAGGGAAAAGCGCCAGATAGGGTGGA 	2538 Db 2280	2479 GTATATTACCGAGCGCTGTACCCCTTTGAATCCAGAAGTCACGATGAGATCACCATCCAG :	ĕ ₹
9 ACTGGTCCCGAACAACTCACCCTGGCTCCTGGGCACGTGATTCTGATCCGGAAAAAGAACAAC		CCCTGGTCTACCACAGAGAAAGGCCCGCTTACCATTTCTGCACAGGAGAGTGTAAAAGTG	ਲੋਂ ₹
9 AAAACAGGAGTTTAGGAAAAAAACCTGAAATTGCCCAGGTTATTGCTTCCTACGCTGCT 	2418 Qy 2160 Db	2359 GACAAGCAGAAGTCGGCTTTTCCATCCGCATCAGGAGCCAGCTAAGCTGGCCACCCAGGCA :	ਲੋਂ ਵੱ
9 GGAGTCTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGCTGGG 	2358 Db 2100		ਲ ₹
GTGATTGTGGTTACCAAGAAAGATGGTGACTGGTGGACGGGAAACGGTGGGCGACAAGTCC	2298 Db	2239 GAGCATGTGCAGCAGGAGGAGGAGCAGCCACGCCCCGGAAACCCCCACGAGGAG	ਲੋਂ ਵੱ
ATTGCCATGTACACATA CGAGAGTTCTGAGCAAGAGATTTAACCTTTCAGCAAGAGGATTTAACCTTTCAGCAAGAGGATTCAGCAAGAGATTCAGCAAGAGATTCAGCATGTACAAGAAGAGTTCTGAGCAAGAGAGATTTAACCTTTCAGCAAGAGGAGATTCAGCAAGAGGAGATTCAGCAAGAGAGATTCAGCAAGAGGAGATTCAGCAAGAGAGAAGATTCAGCAAGAGAGATACAGAGAGAG	2238 Db	2179 TTAGAGAAGCAAAAGGAAGCCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTG :	ਝ ਝ
GETAGNETIANGAGAGASIGGELIC CECEGECEGECAAGECAGECATTCCCGGGGAGAAGAGTTT GETAGTCTAAAGAGAGTGGCTTCCCCGGCCGAGGCCATTCCCGGAGAAAGAGTTTT GETAGTCTAAAGAGAGTGGCTTCCCCGGCCGAGGCCATTCCCGGAGAAAGAGTTTT	2178 Db	2119 CAGAGGTCCCTGGAGGCAGCGCGACTGAAGCAGAAAAAAGAGCAGGAGAAGAAGAGCCTGGAG :	ਝ ਝ
CICATIT CAGGGC CUSTAAGSAMA IC CACANGCA ICUATAC ISGCC LAC ISMANS ICUATAC ICUATAC ISGCC LAC ISMANS ICUATAC ICUATAC ICUATAC ISGCC LAC ISMANS ICUATAC IC	2118 Db	2059 GTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAG :	ਝ ਵ
ATGTGGTGGTGTTGGAGAAGTTCAAAGGTCAGAAGGGTTGGTT	2058 Db		ਰੌ ਵੇ
AAAGACACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGAGAAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGAGAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGAGAGAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGAGACAGCAG	1998 CY 1740 Db	1939 AGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAGGAGCTGGCCCGGCAGCAG :	ਲੋਂ ਵੇ
GGCCAGGGTGAAAAGGTGGAAGGGCTACAAGGGCAAGCCCTGTATCCCTGGAGAGCCAAA	1938 Db	1879 ATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCAT:	ुं द
	878	1819 GCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTT 1	ਲੇ ਵੱ

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                                                                                                                                                                                                The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocytosis). (I) are involved in regulation of clathrin-CC mediated endocytosis (as a complex with Espl5 protein), vesicular CC trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, CC mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); CC sequences antisense to the (I) polynucleotide; agents that downregulate expression of Ese genes or antagonists of an Ese binding partner are CC used to treat diseases associated with undesirable endocytosis and CC resulting changes in cellular function. Particularly overexpression of CE selected cells. (Ant)agonists of (I) is used to promote endocytosis of CC selected cells. (Ant)agonists of (I) or Ab are used to propose abnormal CC proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in CC vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding CC cancer; abnormal cell division or migration; viral infection; or abnormal CC receptor signalling, tissue development or synaptic transmission. The present sequence represents mouse Esell coding sequence.
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                                                                                 Query Match
Best Local Similarity
Matches 3640; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; 88.
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 59-62; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid of endocytosis, \(\text{\chi}\)
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05-FEB-1999;
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                          ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTTGGATGTCTGGGGCCATAACTGTGGAG
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                                                                                                                                                                      1447 A; 1298 C;
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241	ם אם	2419 CCCTGGTCTACCACAGAGAAAGGCCCGCTTACCATTTCTGCACAGGAGAGTGTAAAAGTG 2478 .	B 8
181	ם ס	2359 GACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGCTAAGCTGGCCACCCAGGCA 2418	B 8
121	ov pp ;	2299 AAGAGGGAAGACAGTGTCAGGAAGAAGAGGGGGGAAGAGAGAG	B 8
33.79 GGAGTCTTCCCTTACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGCTGGGG 3438	0	2239 GAGCATGTGCAGCAGGAGGAGGAGCAGCCCCCCGGAAACCCCACGAGGAG	B 8
259	€ B &	2179 TTAGAGAAGCAAAAGGAAGACGCTCAGAGACGACTTCAGGAAAGGGACAAGCAATGGCTG 2238	B 8
199	Db Qy	2119 CAGAGGTCCCTGGAGGCAGGCGCGACTGAAGCAGAAAGAGAGAG	당 성
139	d dd Ad	2059 GTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAG 2118 	B 8
079 821	dg Vy	1999 CTCCGGGAGCAGCTGGACGAGGTGGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGAT 2058 	B 8
761	, B &	1939 AGAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGAGGCTGGCCCGGCAGCAG 1998 	B 6
701	⊋ B 4	1879 ATTCCAGAGAAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCAT 1938 	용 성
641) Db 4	1819 GCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTT 1878 	용 성
	S	1759 CGACTGGCAACCCCAGAGGCAAGAAATTGAGAGGCACGAACAAGTCTAGAGAGACTAAGAATT 1818	B 8
	Q Q	1699 TTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGGTGT 1758 	용 성
	? B &	1639 AACAAGGAGGAGGACGCCCTGGTCCTGAAGGCAAGGAAGAACTCTGGAGTTTGAG 1698	용 성
659 GAGGTTCCCACTCCAGCCAAACCAGTGACCGGTTGACATCTGCCCCTGCCCCCCAAACTG	o da q	AGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTGAATC 	B 8
599 GAGCTGAAAGGAAAACGGGATGCTTCCCTGCAAACTATGCAGAAAAAGATTCCAGAAAAT 	Q y	AGAGGAGGAAGATCGAGAGGCGCGAGGCC 	B &
539 CCAGGAGATATAGTICATGGTIGGATIGAAGCCAGACTGGAGGACCAGGATIGGCTTIGGAGGA [β & &	1459 GAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAGCAGCGGGAGCTGGAGCCG 1518	문왕
	da	1399 CGGTTCGCTCAGCTGGAGCGCCCGAGCAGGAGAGGAGAG	B 8

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               This is the nucleotide sequence of full-length cDNA (clone 21) corresponding to a novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3DIA gene maps to the
                                                                                                                                                                                                            Nucleic acid from the human SH3D1A gene and its products, useful the diagnosis and treatment of myeloproliferative disorders and
                                                                                                                                                                                                                                                                        WPI; 1999-633829/54.
P-PSDB; AAY32155.
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                                                                                                                                             Claim 2; Fig
                                                                                                                                                                                          leukaemia
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diagnosis; therapy;
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Best Local Sim
Matches 4278;
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                                                                                                                                                                                                                                                                             GGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTC
CATTCCAGTTGTTGGAATGTCTCCAACCCTAGTATCTTCTGTTCCCACAGCAGCTGTGCC
                              CATTCCAGTTGTTGGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCC
                                                                                                                                                                                                                                                   GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC
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                                                                                                                         TATAGGAGGGATTGCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTC
                                                                                                                                                              TGCACTTCCCCCTGTCATGAAACAGCAACCAGTTGCTATTTCTAGCGCACCAGCATTTGG
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megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder on chromosome 21, low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities, dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DlA gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk
progress or megakaryoctyic abnormality, myeloproliferative ditacematopoletic disorder, platelet disorder or leukaemia; and haematopoletic disorder (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, leukaemia or neural disorder using a nucleic acid that expresses SH3DIA or its antisense nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing of 5 different sizes of cDNA clone from foetal brain (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                    disorder,
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5458 BP; 1671 A; 1201 C; 1307 G; 1279 T; 0 other;

Similarity GAGGAGGAGTGGAGCGCGCGGGAGGGCGCAGCTTGGTTGCTCCGTAGTACGGCGGCT egganegrerecegeciecegeacrecegecerrecece-ecegecerecegerecacrea GAGAAGAGTGGAGGCGCCAGGGGAGGGAGCGTAGCTTGGTTGCTCCGTAGTACGGCGGCT TTTGTGTGAGGGGGGGCGCGCGCACCCGGCCCGGAGATGAGGCGTCGATCAGCAAGGTGA GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCAGCGGCGCGCGTGAGCGGCACTGA Conservative 69.4**%**; 83.7**%**; 0, Score 3529.4; Pred. No. 0; Mismatches 766; Indels DB 20; Length GACAGAGAGGCGGGCG 69; Gaps 185 245 193 126 84 66 133 22;

253

725 673 665 605

553

613

545

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	TCAGGATATCAGGTGTCGACTGGCAACCCAGAGGCAAGAATTGAGAGCACGAACAAGTC 	683 GACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACT 1	623 ACTCCTGAATCAGAGGAACAAGAGCAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAA 1 	563 CGCAAAACGGGAACTGGAAAGGCAGCGACACTTGAATGGGAACGGAACCGGAGACAGGA 1 	03 GCGGGAGCTGGAGCGGCAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAG	1443 GGAGCGCCAGGAGCAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCA 1502 	1383 GCGCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGCCGCCGAGGAGAGGAAAGAAGG 1442 	1323 GAACTTCGAGCGAGGCAGTGTGGAGCTGGAGAGAAGCGCCCAAGCGCTCTTGGAGCAAGCA	1266 GGATGAGCAGCCAGAGAAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGA 1322 1274 AGATGAACAACAACTAGAAAAGAAATTACCTGTAACGTTTGAAGATAAGAAGCGGGA 1333	06 G	GCCCGTCCTGCCTCCAGAATACATCCCTCCTTCCTTCA		GGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGC 1	966 GAGTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCA 1025 	906 TGTGCCTCAGTCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTAT 965 	846 TAAGTTACAGAAGGCACAATCATTCGATGTCGCCAGGCCCCTCCAGCAGAAGAATGGGC 905	6 AGCCACATGGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACAC	726 TCCCCTGGCTAACGGGGCTCCTCCCGTCATACAGCCTCTGCCTGC
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2865 GCCTTCTCTGACCGTACCTAGTGCTGGCCAGTTACGGCAGAGATCAGCCTTTACCCCAGC 2924	GTGGCCCAGCAGCTCAAACGAAAGCAGAAACGGACAACTGGGATACGTGGGCGGCTCA	2745 GCCAGTGACCTCTTCTGAGCCCTCCACAACCCCCAACAACTGGGCAGACTTCAGTTCCAC 2804	2685 GACCGATCTGACATCTGCCCCTGCCCCCAAACTGGCTCTGCGTGAGACCCCTGCTCCTTT 2744	2625 CCCTGCAAACTATGCAGAAAAGATTCCAGAAAATGAGGTTCCCACTCCAGCCAAACCAGT 2684	2565 AAGCCAGACTGGAAACCCAGGATGGCTTGGAAGAGCTGAAAGGGAAGACGGATGGTT 2624	20 CGATCAGATCACCATCCAGCCAGGAGATAACTCAT	2460 ACAGGAGAGTGTAAAAGTGGTATATTACCGAGCGCTGTACCCCTTTGAATCCAGAAGTCA 2519	TAAGCCAGCACCAGGCACCCTGGTCTACCACAGAGAAAGGCCCGCTTACCATTTCTGC TAAGCCAGCTGTCCAGGCACCCTGGTCCACTGCAGAAAAAGGTCCACTTACCATTTCTGC	AGCCAAACCGGAAATGCAAGACAAGCAAGCAGTTTTCCATCCGCATCAGGAGCCAGC	CCACGAGGAGACAGACTGAAGAGGGAAGACACTGTCAGGAAGAAGGAGGCGGAAGAGAGAG	GANCHARCHATGGCTGGAGCATGTGCAGCAGGAGGAGCAGCCACGCCCCGGAAACC 				GCTGGCCGGCAGCAGCTCGGAGCTGGACGAGGTGGAGGAGGAGGACCAGGTCAAA	GCAGAACAGTTTGCATACAGACTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGA		

5002 TGTGTGTTAACTTGTGCTGTAGCTGAAGCCCGTGTGTCCTTAGATATTAGTTGGAAGT	4	945	Ś
4942 TTTTTAACTAGACTGTGGGGGTTGCTACAGATTAATATGAAATGGCGCTCCTGGTCCGTG	CCCAGCCAGCAATGAATCATATGTTGTCCATCCCCCCTCAGGCTTGAAAGTCCTCAAA 3944	3885 CCCCAGCCAGCAATGAATCATA	유 성
4882 CTTCTTGACAAGAATGTATAGAAGTCTCCCTGCAATTAATT	AGTCAGTGGGCAAGTTGGGCTCTTCCCATCCAATTATGTAAAGCTGACCACAGACATGGA 3884	3825 AGTCAGTGGGCAAGTTGGGCTC	B 8
	CAGCAAAGGCCAGATCATCAACGTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGAGA 3824	3765 CAGCAAAGGCCAGATCAAC 3794 CAACAAGGGCCAGATCATCAAC	당 성
	GTGTGCCAGGTGATCGGGATGTACGATTACACCGCCCAGAACGATGACGAACTAGCCTT 3764	3705 AGTGTGCCAGGTGATCGGGATC	9d 8
	AAGCCCCGGAACAAGCAAAATCACCCCAACTGAGCTACCCAAGACCGCAGTGCAGCCAGC	3645 AAGCCCCGGAACAAGCAAAATC 	g 8
4654 AGTGACCTTGTAGCCACCTAGGAAGCAC-CCATGTTTCCGTTTGGTCTCAGATGTACCT 4712 1	GCAAGCTCGAGGGAAAAAGCGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCT 3644	3585 GCAAGCTCGAGGGAAAAAGCGG	B 8
	TCCTGGGCAGCTGATTCTGATCCGGAAAAAGAACCCCAGGTGGATGGTGGGAAGGAGAACT 3584	3525 TCCTGGGCAGCTGATTCTGATC	d dd
	TGAAATTGCCCAGGTTATTGCTTACGCTGCTACTGGTCCCGAACAACTCACCCTGGC 3524	3465 TGAAATTGCCCAGGTTATTGCT	g 4
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	TGACTGGTGGACGGGACAGGTGGGCGACAAGTCCGGAGTCTTCCCTTCTAACTATGTGAG 3404	3345 TGACTGGTGGACGGGAACGGTC	용왕
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	GGCCGCCAAGCCAGTCCCCGGAGAAGAGTTTATTGCCATGTACACATACGAGAGTTC 3284	3225 GGCCGCCAAGCCAGCCATTCCC	8 8
	CACAAGCATCGATACTGGCCCTACTGAAAGTCCTGCTAGTCTAAAGAGAGTGGCTTCCCC 3224	3165 CACAAGCATCGATACTGGCCCC 3194 TACAAGCATGGATTCTGGTTCT	용 성
4214 AAATTGACTTTCCCCCACCTTTGCACAGGTGCTTTCAATAGTTTTTAAAATTATTTTTAAA	CAGAAGGGTTGGTTCCCCAAGTCTTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATC 3164	3105 TCAGAAGGGTTGGTTCCCCAAC	8 8
4154 GAGCADADATTACCADADACACACAGGGTAGTGGGTCCTTTTGTGGCTTTCCTAGTTACTC	AAGTGACGTCATCACCGTTCTGGAACAGCAAGACATGTGGTGGTTTGGAGAAGTTCAAGG 3104	3045 AAGTGACGTCATCACCGTTCTC	B 8
ACCICATION COLLABOLISTA CONTROL CONTROL CONTROL COLLABORATION ACCICATION CONTROL CONTR	CAAGCGCAAGCCCTGTATCCCTGGAGAGCCAAAAAAGACAACCACTTAAATTTTAACAA 3044 	2985 ACAAGCGCAAGCCCTGTATCCCTW 3014 ACAAGCTCAAGCCCTATATCCTTW	B Q
1000 1000 1000 1000 1000 1000 1000 100	CACAGCCACTGGCTCCTCCCCATCTCCCGTCCTGGGCCAGGGTGAAAAGGTGGAAGGGCT 2984	2925 CACAGCCACTGGCTCCTCCCCA 	B &
3974 GAGACCCACTATCCCCATATCACTGCCCAGAGGGATGATGGGGAGATGCAGCCTTGATCATG 4033		2894 GCCCTCTCTCACCGTTCCAAG	Db

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small candidate region for low platelets on chromosome 21

Sequencing of 5 different sizes of cDNA clone from foetal brain

(see AAZ34570-74) suggests that at least 3 isoforms exist. The

invention provides methods for the diagnosis and treatment of

megakaryocytic abnormality, myeloproliferative disorder, platelet

disorder, acute leukaemia, neural disorders, thromobocytopenia,

platelet disorder on chromosome 21, low platelets in deletion for

21, association of gains in chromosome 21 with leukaemias, neural

abnormalities, dysfunctions and disorders including brain

malformations and corresponding cognitive dysfunctions,

microcephaly, lissencephaly, and colpocephaly. Methods are also

provided for: suppressing cells unable to regulate themselves,

screening for a somatic alteration in the SHBDA gene; monitoring

the progress or megakaryocytic abnormality, myeloproliferative disorder,

haematopoietic disorder, platelet disorder or leukaemia; and

treatment of a subject (including a prenatal subject) having

megakaryocytic abnormality, myeloproliferative disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to a novel human SH3 gene, termed the SH3D1A gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3D1A gene maps to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid from the human SH3D1A gene and its products, useful the diagnosis and treatment of myeloproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-633829/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Korenberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3D1A gene;
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3133 GTGAAACTCATTTCAGGGCCCGTAAGGAATCCACAAGCATCGATACTGGCCCTACTGAA 3192		2056 GATGTTTTCAACAACCAGCTGAAGGAACTGAGAGAGATACATAGCAAACAGCAACTCCAG 2115	`
059 CAAGACATGTGGTTTTGGAGAAGTTCAAGGTCAGAAGGGTTTGGTTCCCCAAGTCTTAC	B *	1996 CAGCTCCGGGAGCAGCTGGACGAGGAGAGAGAGACCAGGTCAAAGCTGCAGGAGATT 2055 	0 \
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939	2 dd 42	1876 CTTATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTG 1935 	• •
CROTTACGGCAGAATCAGCCTTTACCCCAGCCACAGCCACGCCCCCTCCCCCATCTCCCCCCTTTACCCCCCTTTACCCCAGCCACGCCACGCCCACGCCCCCCCTCCCCCCTCTCCCCCCCC	5 p &	1816 ATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGA 1875 	•
833 GAAACGGACAACTGGGATACGTGGGCGCTCAGCCTTCTCTGACCGTACCTAGTGCTGGC	o da	1756 TGTCGACTGGCAACCCCAGAGGCAAGAAATTGAGAGCACGAACAAGTCTAGAGAGCTAAGA 1815 	•
773 ACCCCCAACACTGGGCAGACTTCAGTTCCACGTGGCCCAGCAGCTCAAACGAGAAGCA 	D 64	1696 GAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGG 1755 	•
AAACTGGCTCTGCGTGAGACCCCTGCTCCTTTGCCAGTGACCTCTTCTGAGCCCTCCACA	D	1636 AGGAACAAGGAGGAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAAGACTCTGGAGTTT 1695	•
GANAATGAGGTTCCCGCTCCAGTGAAACCAGTGACTGATTCAACATCTGCCCCTGCCCCC	Db 43	1576 CTGGAAAGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTGAATCAG 1635 	•
SYS GRAGGAGAGCTIGAAGGGAAAGATTCCC SYS GRAGGAGAACGATTCCA SYS GRAGGAGAACGATTCCA SYS GRAGGAGAATTAAAAGGAAAGACGATTCCCTGCAAACTATIGCAGAAAAATCCCA SYS GRAGGAGAATTAAAAGGAAAGACGAGGTGGTTCCCTGCAAACTATGCAGAGAAAATCCCA STORMAN GAAATGAACGAGAGAGAATGAACGAATGAAAATGAAAAATCCCA	S & &	1516 CGGCAGCGAGAGGAGGAGGAGGAGGAGAGTCGAGAGGCCGCAAGACGGGAA 1575 	•
3 ATCCAGCCAGGAGATATAGTCATGGTGGATGAAAGCCAGATGGAGGAGGCAGGATGGCTT 19 ATCCAGCCAGGAGACATAGTCATGGTGGATGAAAGCCAAACTGGAGAACCCGGCTGGCT	, p &	1456 CAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCCAGCTGGAGAAGCAGCAGCGGGAGCTGGAG 1515	• •
AMAGINGGA A A A LACCUMOCUC ISTACCICI I I MAA I CAMAA CACUA I GAGA TCACU	da	1396 GAGCGGTTGGCTCAGCTGGAGCGCGCCGAGCAGGAGAGGAAAAGAGCGGGAGCGCCAGGAG 1455	• •
	o da y	1336 GGCAGTGTGGAGAAGAGCGCCGCCAAGCGCTCTTGGAGCAGCAGCGCAAAGAGCAG 1395 	•
A IGENEGATION CONTINUE TO THE	מם ע	1279 CCAGAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGAGAACTTCGAGCGA 1335 	• `
AGACTIGAAGAGGGAAGACKSTGTCKAGAAGAAGGAGGCGGAAGAGAGGAGGCGGAAGAGGAGGAG	्रे व्य	1219 AGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCGTCGTCAGAGGATGAGCAGCAG 1278	0 \
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GAGTIRAGHAAGCAAAAGAAGCACTCRAGHACGACTGAGGAAAGGAAAGGACAATGG) b 4	1099 CTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCT 1158	0 \
ANGCANANGICC LIGNAGGCAGGCGCGACTGANGCAGAAAGAACKAGAAAAAAAACKC LIG 	2 dg 42	1039 TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATC 1098 	• •
9 GATATTTTCAATAATCAGCTGAAGGAACTAAGAGAAATAACAATAAGCAACACTCCAG	Db	979 ACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCT 1038 	•

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GCTTTCAATAGTTTTAAAATTTTTTTAAATATATATTTTAGCTTTTTAATAAACAAAAT
                      GCTTTCAATAGTTTTAAGATTATTTTTAAATGTGTATTTTAGCCTTTTAATAAAAATCTC
                                                                                                         TGGGTCCTTTTGGGGCTTTCCTAGTCACTCAGACTGAC-CGGCCCCGCCCTTCACACGGGC
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                                                                                           TCCCTGCAATTAATTT - CCAATGTTTACATTTTTTAACTAGACTGT - GGAATTTCTACAG
                                                                                                       TCCCTGCAATTAATTTCCCAGTGTTTACATTTTTAACTAGACTGTGGGGGTTGCTACAG
                                                                                                                                        TTATGGAA-----TATCTTGAACAAGTAATCTTCTTGACAAGAAAGAATGTATAGAAGTC
                                                                                                                                                                                                                                                  AATCTGGCATGTCTTCACACCATAAACTAGTAAGACGCCAACCTGCCCAGGCGGTTACGAT
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 CTGTTTGTCTTTTAAACACTAGTTGGAAGCTCTCAATAAAAT
                                                          ATTAATATGAAATGGCGCTCCTGGTCCGTGTGTGTTAACTTGTGCTGTAGCTGAAGCC
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                                              ATTAATATGAAATGGAGCTCATGGTCCGTTTGTGTGTT
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SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopeniar; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy;

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                                                                                                                                                                                                                                                                                                                                              to a novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, countributes of both in general and in particular those involving the megakaryocytic lineage. The SH3DIA gene maps to the small candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of cDNA clone (see AA234570-74) suggests that cat least 3 isoforms exist. The invention provides methods for the countries of the cou
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Best Local Similarity
Matches 4030; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid from the human SH3D1A gene and its products, useful the diagnosis and treatment of myeloproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig
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ATTGCCCAGGTTATTGCCTCATACACCGCCCACCGGCCCCGAGCAGCTCACTCTCGCCCCT	Qy 2389 CAGGAGCCAGCTAAGCTGGCCACCCAGGCACCCTGGTCTACCACAGAGAAAAGGCCCGCTT 2448
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	Oy 2152 AAAGAGCAGGAGAGGAAGAGCCTGGAGTTAGAGAAAGGAAGAGCGAAGACGA 2211 7 Ob
ACCAAGCCAGCCATTCCCCGGAGAAGAGTTTATTGCCATGTACACATACGAGAGTTCTGAGCCCCCAGCA	Qy 2092 ATACATAGCAAACAGCAÁCTCCAGAAGCAGAGGTCCCTGGAGGCAGCAGCAGCAGCAG 2151 Db
3109 ANGGGTTGGTTCCCCANGTCTTACGTGAAACTCATTTCAGGGCCCATAAGGAAGTCTACA 3123 3064 ANGGGTTGGTTCCCCAAGTCTTACGTGAAACTCATTTCAGGGCCCATAAGGAAGTCTACA 3123 3064 ANGGGTTGGTTCCCCAAGTCTTACGTGAAACTCATTTCAGGGCCCATAAGGAAGTCTACA 3123	QY 2032 ACCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTGAAGGAACTGAGAGA 2091 U 1
049 GACGICAICACCGITCTIGGAACAGCAGGAGACATGICGTGGTTTGGAGAGAGTTCAAGGTCAG	OY 1972 GAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCGGGAGCGAGC
	Oy 1912 AAACAAGTCCAGGAGAACAGTTTGCATAGAGACTCGCTTCTTACCCTCAAAAGAGGCCTTG 1971
CUCATION CONTROL CON	Qy 1852 GAATCTCAGCAAATGCTTGGAAGACTTATTCCAGAGAAACAGATACTCAGTGACCAGTTA 1911 Db 1804 GAATCTCAGCAAATGCTTGGAAGACTTATTCCAGAAAAACAGATACTCAATGACCAATTA 1863
	Oy 1792 ACGAACAAGTCTAGAGAGCTAAGAATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAG 1851 V Db 1744 ACAAACAAATCTAGAGAGTTGAGAATTGCCGAAATCACCCATCTACAGCAACAATTACAG 1803 Db
	Qy 1732 GAAGGAAAACTTCAGGATATCAGGTGTCGACTGGCAACCCAGAGGCAAGAAATTGAGAGC 1791 U
704 GTAACCTCTTCAGAGCCCTCCACGACCCCTAATAACTGGGCCGACTTCAGCTCCACGTGGCCCTGGACCCCTGGACCCCTGGACACTTCAGCTCCACGTGGCCCTGGACACTTCAGCTCCACGTGGACTCCACGTGGACTTCAGCTCCACGTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACACGTGGACTGACT	Qy 1672 GCAAGGAGGAGAAGACTCTGAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTA 1731
644	Qy 1612 CGGAGACAGGAACTACTGAATCAGAGGAACAAGAAGAACAAGGAGGAGGAGGCACCGTGGTCCTGAAG 1671 UY CGAAGGCAAGAACTACTAAATCAAAGAACAAGAACAAGAACAAGAGACATAGTTGTACTGAAA 1623 Db
	Oy 1552 AGGCGCGAGAGCCGCAAAACCGGAAACTGGAAAACGCAACCTTGAATGGGAACCGAAC 1611
50 CANACTORANCE CONTROL	Qy 1492 CTGGAGAGCGGGAGCTGGAGCGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
	Qy 1432 AGGAAAGAGCGGGAGGCCAGGAGCAGGAGGCAAGCCAGCTGGAGCTGGAGAAGCAG 1491
404	Oy 1372 TTGGAGCAGCAGCAGAAGAGCAGGAGCAGGTTGGCTCAGCTGGAGCGCGCCGAGCAGGAG 1431 Db 1411
2344 CAAGAACCAGCTAAGCCAGCTGTCCAGGCACCCTGGTCCACTGCAGAAAAAGGTCCACTT 2403 2449 ACCATTTCTGCACAGGAGAGTGTAAAAGTGGTATATTACCGAGCGCTGTACCCCTTTGAA 2508	Db 1264 AAGAAGCGGGAGAACTTTGAACGTGGCAACCTGGAACTGGAGAACGAAGGCAAGCTCTC 1323 Qy

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                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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food supplement; medical imaging; diagnostic;
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CC Mote: The sequence data for this patent did not appear in the printed CC at ftp.wipo.int/pub/published_pct_sequences.
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ABK43498 standard; CDNA;

3319 ВP

05-JUN-2002 (first entry)

encoding novel central nervous system protein #78.

RESULT 10
ABK43498
ID ABK43
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AC ABK43
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DT 05-JI
XX
DX Cent
KW Cert
KW Carc
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DS Hor
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D hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; leukaemia; neovascularisation; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss. 17-JAN-2001; 2001WO-US01332 02-AUG-2001. Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;

31-JAN-2000; 2000US-0179065

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02-OCT-2000

02-OCT-2000

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08-NOV-2000

09-DEC-2000

09-DEC-2000

08-DEC-2000

ew isolated nucleic acid encoding a preventing, treating or ameliorating food additives or preservatives -
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P-PSDB; AAU87168.
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16-MAR 2000
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21-MAY 2000
22-JUIN 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases e.g. rheumatoid arrhiritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzhaimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. corneal infection, gastrointestinal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include
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                                                              CAGTGCCAATGGGATCCATTCCAGTTGTTGGAATGTCTCCAACCCTAGTATCTTCTGTTC
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                              GGCAAGAAATTGAGAGCACGAACAAGTCTAGAGAGCTAAGAATTGCTGAAAATCACCCACT 1834
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PR 02-MA
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Best Local Similarity
Matches 1832; Conserv
                                                                                                                                                                                                                                                                      The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
                                                                                                                                                                                                                                              Sequence 2131 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830 Primers useful for synthesizing use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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DB; AAM93229.
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su A, Sugiyama
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AGCGGCGCGTGAGCGGCACTGATTTGTCCCTGGGGCGGCAGCGCGGACCCCGCGCGAGAT
                      SEQ ID NO 2646; 1380pp +
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na T, Nagai
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Pred. No. 0;
                                                                                                                                                                                                                                            C; 526 G; 442 T; 0 other;
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K, Kojima
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T, Koga
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CATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGAGGCAGTGTGGAGCTGGAGAAGCGCC 1360
                                               TGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAGC---CAGAGAAAAACTGCCTGTGA 1300
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AAZ34573 standard; cDNA; 묤

01-FEB-2000 (first entry)

Human SH3D1A cDNA clone

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RESULT 12
AAZ34573
ID AAZ34
XX AAZ34
AC AAZ34
XX O1-FE
XX U1-FE
XX Human
XX SH3DI
KW megak
KW plate SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia;

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CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary trand of a polynucleotide which complementary the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises a type of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination CC oraplementary strand of a polynucleotide which comprises a 5'-end sequence complementary to the CC onlynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises a 1'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and CC in gene therapt of The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow-obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH13742 represent human cDNA sequences; AAB92446 to AAH3633 represent human amino acid sequences; and AAH13629 to AAH13632 of the present inventions.
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02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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Sugiyama T, Wakamatsu
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                                                                                                                                                                                                           GAGGAGGAGTIGGAGCGGCGCGGAGGGGCAGCTTTGGTTGCTCCGTAGTACGGCGGCG
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ACGTAATAGAACCATGGCTCAGTTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGC 305
                                                                                                                                                                                        CGCGAGGAAGAATCCCGAGCGGGCTCCGGGACG
                                              TTTGTCCCTGGGGCGGCAGCGCGGACCCCGCCGGAGATGAGGCGTCGATTAGCAAGGTAA
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C, Otsuki
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SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; th sapiens

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                          cc small candidate region for low platelets on chromosome 21.

cc Sequencing of 5 different sizes of cDNA clone from foetal brain cc (see AAZ34570-74) suggests that at least 3 isoforms exist. The cinyention provides methods for the diagnosis and treatment of invention provides methods for the diagnosis and treatment of comparation provides methods for the diagnosis and treatment of comparation provides methods for the diagnosis and treatment of comparation contromosome 21, low platelets in deletion for comparations and corresponding compitate the leukaemias, neural abnormalities, dysfunctions and disorders including brain comparations and corresponding compitive dysfunctions, compared for a sometic alteration in the SHDDA gene; monitoring the progress and adequacy of a treatment; monitoring tunour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, chaematopoietic disorder, platelet disorder or leukaemia; and comparation subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, leukaemia or neural disorder using a contract of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder.
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 2359; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9) corresponding to a novel human SH3 gene, termed the SH3DIA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3DIA gene maps to the
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3231 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid from the human SH3D1A gene and its products, useful the diagnosis and treatment of myeloproliferative disorders and
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   GGAGCAGCTGGACGAGGAGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGATGTTTT
                                                              CTCGCTTCTTACCCTCAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCG
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                                                                                                          AGAAAAACAGATACTCAATGACCAATTAAAACAAGTTCAGCAGAACAGTTTGCACAGAGA
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                                                     AGACAACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGACAT
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Human;	KW	1968 TTTGTGGCTTTCCTAGTTACTCAAATTGACTTTCCCCCACCTTTGCACAGGTGCTTTCAA 2027	망
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AAS847	48 8	4101 CTGAGTCACTGCGTGCAGAGGCAGAAGCAAATTGCAGAACTGCACAGGGTGGTGGTGGTTCCT 4160	ş
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ULT 15	RES	4041 GAAGAACTCACTGCAGAGCAGTTTACCTCATTTGACCTTAGTTGCATGTGATCGAAATGT 4100	ş
28	Db	1963 1962	망
. 50	. Q	3981 ATGGGAGATGCAGCCTTGATCATGTGACTTGCAGCATGATCACCTACTGCCTTCTGAGTA 4040	Ś
27	Db Db	1948 CCCTCAGGCTTGAAA 1962	Ф
49	γQ	3921 CCCTCAGGCTTGAAAGTCCTCAAAGAGACCCACTATCCCCATATCACTGCCCAGAGGGATG 3980	Ş
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49	γQ	861 TGTAAAGCTGACCACAGACATGGACCCCAGCCAGCAATGAATCATATGTTGTCCATCCCC	ş
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48	νQ	GGACCCGGACTGGTGGAAAGGAGAAGTCAGTGGGCAAGTTGGGCTCTTCCCATCCAATTA	ફ
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48	δ	CCAGAACGATGACGAACTAGCCTTCAGCAAAGGCCAGATCATCAACGTCCTCAACAAGGA	Ş
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47	δ	3681 ACCCAAGACCGCAGTGCAGCCAGCAGTGTGCCAGGTGATCGGGATGTACGATTACACCGC 3740	ঠ
25	da	1648 CCCAGCTAATTATGTAAAGCTTCTAAGCCCTGGGACGAGCAAAATCACTCCAACAGAGCC 1707	ф
46	8		Ş
24	da	1588 AGGTGGATGGTGGGAAGGAGAGCTGCAAGCACGTGGGAAAAAGCGCCAGATAGGCTGGTT 1647	Дb
46	δδ	3561 AGGTGGATGGTGGGAAGGAGAACTGCAAGCTCGAGGGAAAAAGCGCCAGATAGGGTGGTT 3620	ş
23	Д	1528 CGGCCCCGAGCAGCTCTCCGCCCCTGGTCAGCTGATTTTGATCCGAAAAAAGAACCC 1587	Дb
45		3501 TGGTCCCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTGATCCGGAAAAAGAACCC 3560	Ş
23	מט	1493	рь
4. c	; 5	3441 AACAGGGAGTTTAGGAAAAAACCTTGAAATTGCCCAGGTTATTGCTTCCTACGCTGCTAC 3500	Ş
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4.4	. S	3381 AGTCTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGGAACTGCTGGGAA 3440	Qγ
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. 4	, 1 ₀	3321 GATTGTGGTTACCAAGAAAGATGGTGACTGGTGGACGGGAACGGTGGGCGACAAGTCCGG 3380	Ş
	, 6	1493 1492	В
	; 5	3261 TGCCATGTACACATACGAGAGTTCTGAGCAAGGAGATTTAACCTTTCAGCAAGGGGATGT 3320	Ş
20) D	1441 TAGTCTAAAGCGAGTAGCCTCTCCAGCAGCCAGCCGGTCGTTTCGGGAGAA 1492	Db .
42		3201 TAGTCTAAAGAGAGTGGCTTCCCCGGGCCGAGCCAAGCCAATTCCCCGGAGAAGAGGTTTAT 3260	Ś
. 20	σb	1381 CATTTCAGGGCCCATAAGGAAGTCTACAAGCATGGATTCTGGTTCTTCAGAGAGTCCTGC 1440	Db
42	Ş	3141 CATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCTGC 3200	Ş
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CTTTTAAACACTAGTTGGAAGCTCTCAATAAAAAT 2892
                                              TCCACAGTCTCTTTTAGTCTCTGTTACATGAAGTTTATTCCAGTTACTTTTCATGGAA
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Human; chromosome mapping; gene mapping; gene therapy; forensic;

DNA encoding novel human diagnostic protein #20566

13-FEB-2002 AAS84762;

(first

entry)

AAS84762 standard; cDNA; 2874

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                                                                                                                                                                                                                                                                                                                                                                                          cc polypeptide (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The cc polynucleotides are also used in diagnostics as expressed sequence tags cc for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. Cc The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and activity cand to produce other types of data and products dependent on DNA and cc amino acid sequences. AAS64197-AAS94564 represent novel human cc diagnostic coding sequences of the invention.

Cc note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at this patent did not appear in the printed specification, but was obtained pot_sequences.
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Best Local S
Matches 1778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

				Result No.
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804.2	809.8	1582	1598.2	Query Score Match Length DB ID
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906	818	2079	2126	Length
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BU519029	CA324450	BC013578	BC020269	DB ID
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CB524 CB52 CBM945 CB52 CB52 CB52 CB52 CB52 CB52 CB52 CB5

ALIGNMENTS

REMARK COMMENT	REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 BC020269 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2126) Strausberg,R. Direct Submission Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	BC020269 2126 bp mRNA linear HTC 19-DEC-2001 Homo sapiens, clone IMAGE:4899011, mRNA. BC020269 BC020269.1 GI:17939664 HTC. Homo sapiens (human)

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                                                          CCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTTGGAATGTCTCCA
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                 Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.llr Series: IRAK Plate: 14 Row: c Column: 5
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 4
This clone has the following problem: retained intron.
                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                       USA
NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technolog
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                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                   TGCTTGGAAGACTTATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCAGC
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818 bp mRNA linear UI-M-FY0-ccl-a-05-0-UI.rl NIH_BMAP_FY0 Mus musculus IMAGE: 6820974 5', mRNA sequence.
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1 (bases 1 to 818)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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The following repetitive elements were found in
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                                                                                                                     /clone="IMAGE: 6820974"
/tlissue_type="whole brain"
/dev stage="membryo 13.5,14.5,16.5,17.5dpc"
/lab_host="PH108 (T1 phage resistant)"
/clone_lib="NHH_BMAP_FY0"
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/clone_lib="NHH_BMAP_FY0"
/clone="Department of the library was constructed according
site_2: Not 1; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the NotI site and the polyA tail
is AGCAGAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
270 g 127 t 4 others
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/strain="C57BL/6"
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Unpublished
Contact: Robert Strausberg,
                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Plate: LLMM14095 row: o column: 18
High quality sequence stop: 701.
Location/Qualifiers
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Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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AKOB2606 LOCUS DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230068L04 product:Intersectin (SH3 domain protein 1A), full insert sequence. ACCESSION AKOB2606 VERSION KENORCE ORGANISM Mus musculus (house mouse) ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. REFERENCE 1 AUTHORS Carninci, P. and Hayashizaki, Y.	Qy 1596 TGAATGGGAAC-GGAACCCGGAGACACGAATCAGAGAACAAGAACAAGAGAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACAAGAACACAGAACAAGAACACAGAAGA	Qy 1296 TGTGACATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGAG	Qy 1056 TGACATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATCCTAGCTATGCACCTAAT 1115

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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2589)
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                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium and the RIKEN Genome Exploration Research
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URL:http://fantom.gsc.riken.go.jp/.
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/tybesseggdlifeqqgvivvvkkdgdmwtgtggdksgyprayvrikdsbegsgtagk
rtgslckkpeiaqviasyaatgpeqlitlapgdlitlikkkppggwregelqarkxgqg
rfpanyvkllspgtskitptektavppavqqvigmydytaqnddelapskgqiinv
lnkeddpmwkcbysgqyglepsnyvklitdmdbeqqwcsdlhillitpterkgqqiinv
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lnkeddpmwkcbysgqyglepsnyrklitresellitekaaliqoktdbapappkepvk
rkkonsgekmpvkmigdilsaqlphmqpyirfcentpenpphehlkhalekael
csqvnegvrekensdrlemiqahvqceglseqlvfnsvtnclgprkflikgklykaks
nkelygflyndflitroitkplgssgtjkvpsprsniqykmyktpiflensvlkkael
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/clone_lib="RIKEN_full-length_enriched_mouse_cDNA_library"
/dev_stage="0_day_neonate"
<1. .2269</pre>
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Gequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contribution:
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 732)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CA750495.1 GI:25575732
EST.
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UI-M-FY0-cde-p-10-0-UI.r1 NIH_BMA
IMAGE: 6832091 5', mRNA sequence.
                                                                                                                                                                                                     The following repetitive elements were found in this cDNA sequence: 637-722, >(CAG)n#Simple_repeat
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                                                                                                                                                                                        primer: pYX-5.
/mol type="mRNA"

/strain="057BL/6"

/db_xref="taxon:10090"

/dlone="IMAGE: 6832091"

/tissue_type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP FY0"

/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                            organism="Mus musculus"
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Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyx.Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACACA. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

Ouery (Ouery	Query Match 14.3#; Score 727.2; DB 14; Length 732; Best Local Similarity 99.6#; Pred. No. 1.4e-148; Matches 729; Conservative 0; Mismatches 3; Indels 0; Gaps 0; 788 CCACATGCCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTA 847
	088 AAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGC
ŕ	B CCGTCCTGCCTCCAGAATACATCCCTCCTTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGA
,	8 TGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGGAGCCGTCGTCAGAGG
ъ 4	1268 ATGAGCAGCAGCAGAGAAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAACT 13
ĕ ₹	1328 TCGAGCGAGGCAGTGTGGAGCTGGAGAGAGCGCCCAAGCGCTCTTGGAGCAGCAGCGCA 1
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Matches 724
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TITLE
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CB248849.1 GI:28387663
EST.
Mus musculus (house moust
Mus musculus
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian
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VI-M-EXO-byj-m-24-0-VI.r1 NIH BMA
IMAGE: 5719103 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 725)
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                       GACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGGTGTCGACTGGCAACCCCAG 1773
                                                                                                                      GGCACCGTGGTCCTGAAGGCAAGGAGGAAGACTCTGGAGTTTGAGTTAGAAGCTCTGAAT 1713
                                                                                       GGCACCGTGGTCCTGAAGGCAAGGAGGAAGACTCTGGAGTTTGAGTTAGAAGCTCTGAAT 120
                                                                                                                                                                               CTTGAATGGGAACGGGAGCAGGAACTCCTGAATCAGAGGAACAAGGAGCAGGAG
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GACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGGTGTCGACTGGCAACCCAG
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                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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/dev stage="embry 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone lib="NHH BMAP EXO"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 5719103"
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                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 732)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1. .732
/organism="Mus musculus"
                                          location/Qualifiers
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/tlissue_type="whole brain"
/dev_stage="embryo 18.5 dpc"
/lab_host="DHIOB (TI phage resistant)"
/clone_lib="NIH_BVAP_EHOp"
/clone_lib
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Pred. No. 1.
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1.3e-147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 738)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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UI-M-EHOp-bvr-j-08-0-UI.r1 NIH E
IMAGE:5695975 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                        198
                                                                                                                                    /tissue type="whole brain"
/dev stage="wembryo 18.5 dpc"
/lab_host="PH108 (TI phage resistant)"
/clone_lib="NIH_BMAP_EHOP"
/clone_lib="NIH_BMAP_EHOP"
/clone_lib="NIH_BMAP_EHOP"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="Torgan: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="Torgan: brain; Vector: pYX-Asc; Site_1: EcoR I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone was contributed by the Brain Molecular Anatomy Project
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14.2%;
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Score 721.2; DB Pred. No. 3e-147;
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Sciurognathi; Muridae; Murinae; Mus
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_BMAP_EHOp Mus musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim.Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
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CB521237.1 GI:29354592
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706 bp mRNA linear EST 28-MAR-UI-M-GH0-cem-g-10-0-UI.rl NIH BMAP_GH0 Mus musculus cDNA clone
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The following repetitive elements were found in this cDNA sequence: 220-337, >(GGA)n#Simple_repeat
Seq primer: pYX-5,
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Rodentia;
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/db xref="taxon:10090"
/db xref="taxon:10090"
/db xref="taxon:10090"
/clone="IMAGE: 6841475"
/tissue_type="whole brain"
/dev etage="1, 5, and 15 days newborn"
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/dev etage="1, 5, and 15 days newborn"
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Query Match
Best Local Similarity
Matches 703; Conserv
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                                                                                                                                 IMAGE: 6849689 (
CB527154
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EST.
1 (bases 1 to 703)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                     CB527154 703 bp mRNA
UI-M-FYO-cfh-m-16-0-UI.rl NIH_BMAP_FYO |
IMAGE: 6849689 5', mRNA sequence.
                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                           Mus musculus
                                                                                                               Mus musculus (house mouse)
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RESULT 11
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AUTHORS
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ORGANISM
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    Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                BU704308.1 GI:23632308
EST.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                               BU704308 729 bp UI-M-FOO-bzs-j-21-0-UI.rl NIH BMA IMAGE: 6406772 5', mRNA sequence.
                                                                                   Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov
                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
I (bases 1 to 729)
                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAACGGGGCTCCTCCCGTCATACAG
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GTTGCCATGTCTGGTCAGCCACCTGCCGCCCGTCCTGCAGAATACATCCCTTCCCTTCCC
                                                                                                                                                                       ATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTTGGCTTCAATATGGAATCTTTCTGAC
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                                                                ATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATCCTAGCTATGCACCTAATTGAT
                                                                                              ATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATCCTAGCTATGCACCTAATTGAT 1119
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/dev stage="embryo 12.5dpc"
/lab_host="DH108 (TI phage resistant)"
/clone_lib="NIH BMAP_FOO"
/clone_lib="NIH BMAP_FOO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGGCC. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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a 206
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/strain="C57BL/6"
/db_xref="taxon:10090"
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Pred. No. 1.2e-143;
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Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of cDNA Library Arrayed by: Dr. M. Bento Soares, University of I
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer:
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TTCCATCCGCATCAGGAGCCAGCTAAGCTGGCCACCCAGGCACCCTGGTCTACCACAGAG 2436
                                                                                                                                               GAGCAGCCACGCCCCGGAAACCCCCACGAGGAGGACAGACTGAAGAGGGGAAGACAGTGTC
                                                                                                                                                                           GAGCAGCCACGCCCCCGGAAACCCCCACGAGGAGGACAGACTGAAGAGGGAAGACAGTGTC
                                                                                                                                                                                                                                              GACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTGGAGCATGTGCAGCAGGAG
                                                                                                                                                                                                                                                                               GACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTGGAGCATGTGCAGCAGGAG 2256
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                                              AGGAAGAAGGAGGCGGAAGAGAGAGCCAAGCCGGAAATGCAAGACAAGCAGAGTCGGCTT
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                                                                                              AGGAAGAAGGAGGCGGAAGAGAGAGCCAAGCCGGAAATGCAAGACAAGCAGAGTCGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev stage="embryo 13.5,14.5,16.5,17.5dpc"
//lab host="DH10B (T1 phage resistant)"
//clone_lib="NIH_BMAP_FYO"
//clone_lib="NIH_BMAP_FYO"
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
//note="Organ: Brain; Vector: pYX- Asc vector: Braind cDNA was size fraction and then cloned with EcoR I adaptor, digested with NotI and then cloned directionally into pYX- Asc vector. The library tag sequence located between the NotI site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
//program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE: 6849689"
/tissue_type="whole brain"
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/strain="C57BL/6"
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Pred. No. 1.8e-142;
Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares,
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA323050 mRNA linear UI-M-FYO-cdc-j-23-0-UI.rl NIH_BMAP_FYO Mus musculus IMAGE: 6827736 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
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CA329050.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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            /clone="IMAGE: 6827736"
/tlisuse_type="whole brain"
/tisuse_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (TI phage resistant)"
/clone=lib="NIH_BMAP_RYO"
/clone=lib="NIH_BMAP_RYO"
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/inte="Corgan: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
with EcoR I adaptor, digested with Ist and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Rrain Anatomy Project (HAMD) 'Gene Digovery in the
                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (Dases 1 to 782)'
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                  BG922629
BG922629.1 GI:14303105
                                                                                                                     602821583F1 NCI_CGAP_Mam6
                                                Mus musculus
                                                                         EST
                                                                                                          mRNA sequence.
                                                          Mus musculus (house
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TITLE
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Best Local Similarity
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Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                          ACTCACTGCAGAGCAGTTTACCTCATTTGACCTTAGTTGCATGTGATCGAAATGTCTGAG 4105
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/tissue_type="infiltrating ductal carcinoma"
/tissue_type="5 months"
/dev_stage="5 months"
/lab_host="DHIOB"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal_Site_2: Not; Cloned unidirectionally. Primer: Oligo d Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
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Search completed: December 5, 2003, 00:39:52 Job time : 6505.62 secs		36 TTGCCTATTTTGGTTTTACAAAAACACCCACTATCAAGGAGTGC 4329	658 TAAGATTATTTGTAAATGTGTATTTTAGCCTTTTTA-ATAAAAATCAATCAATTACTTCT 716	26 TAAGATTATTTTTAAATGTGTATTTTAGCCTTTTTAATAAAAATCTCAATCAA	601 GGCTTTCCTAGTCACTCAGACTGACGGCCCGCTTCACACGGGGCGCTTTCAATAGTTT 657	4166 GGCTTTCCTAGTCACTCAGACTGACCGGCCCCCCCCCCTTCACACGGGCGCTTTCAATAGTTT 4225	

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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6. /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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SEQ ID NO 72
LENGTH: 2017
TYPE: DNA
ORGANISM: Homo sapien
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APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CAN
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
FITTLE OF INVENTION: COMPOSITIONS AND METHODS FO)
FITTLE OF INVENTION: COMPOSITIONS AND METHODS FO)
FITTLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 199-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 2017
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US-09-338-933-72
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RESULT 3
US-09-215-681-72
; Sequence 72, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
; CURRENT PILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 2017
TYPE: DNA
ORGANISM: Homo sapien

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Local Similarity 55.4%;
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Pred. No. 4.3e-116;
0; Mismatches 812;
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RESULT 4
US-08-630-915A-193
; Sequence 193, Application US/08630915A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
PEFFERRICE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2873 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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3227 CCGCCAAGCCAGCCATTCCCCGGAGAAGAGTTTATTGCCATGTACACATACGAGAGTTCTG 3286
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(212) 869-8864/9741
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: SPARKS
                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                    COUNTRY: USA
ZIP: 10036-2711
                                                                                               STREET: 1155 A
                                                                                   STATE:
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                                                                                New York
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                                                                                                                                                                                                                         HOFFMAN, NO. 630
KAY, Brian K.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                      SPARKS, Andrew B.
                                                                                                                                                                     USING SAME
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Sequence 39, Application US/08630915A Patent No. 6309820
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
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                                                                                                                                                                             1155 Avenue of the Americas
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    L, Stephen J.
POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                         6309820h
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Best Local Similarity 63.9%;
Matches 418; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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                              GTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGAAGTCAGTGGGCAAGTTGGGCTC
                                                                                                                                                  TATGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTCTCCAAGGGACAACTCATTAAT
                                                                                                                                                                         TACGATTACACCGCCCAGAACGATGACGAACTAGCCTTCAGCAAAGGCCAGATCATCAAC
                                                                                                                                                                                                                        ACACCTGCCTTTCATCCT--
                                                                                                                                                                                                                                                        ACCCCAACTGAGCTACCCAAGACCGCAGTGCAGCCAGCAGTGTGCCAGGTGATCGGGATG
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                                                                                                                                                                                                                                                                                                                                                                        CTAAAGAAAAATACAAGTGGGTGGTGGCAAGGAAGTTACAGGCCAGAGGAAAAAAAGCGA
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                                                                         GTTATGAACAAAGATGATCCTGATTGGTGGCAAGGAGAGATCAACGGGGTGACTGGTCTC
 TTTCCTTCAAACTACGTTAAGATGACGACAGACTCAGATCCAAGTCAACAGTGA
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RESULT 6 US-09-404-879A-5

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GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

ITILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

ITILE REFERENCE: 210121.46202

CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 393

SOFTWARE: FASCSEQ FOR WINDOWS Version 3.0

SEQ ID NO 5

LENGTH: 531

TYPE: DNA

ORGANISM: Homo sapien

US-09-404-879A-5
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 531
TYPE: DNA
                                                                                                                                                                                                                                                                        RESULT 7
US-09-338-933-5
; Sequence 5, Application US/09338933
; Patent No. 6488931
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATAACCTCAAACCTTCAGGAGGTTACATAACAGGTGATCAAGCCCGTACTTTTTTCCTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTAGCCTGGATGTCTGGGGCCATAACTGTGGAGGAAAAGGGCCAAGCATGACCAGCAGTTC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGGATATCAGCTCCCCTCCACACTTCCCCCCTGTCATGAAACAGCAACCAGTGGCTATT 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAAACTCATCAAGTTAAAGTTG 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCCCACAGCGATGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCCAATCTGTCCATTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGGCCAACAGCTGCCTGTAGTCCTCCTCCTATCATGAAACAACCCC-----CTATG 362
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Pred. No. 1.5e-29;
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                                                                                                                                                                                               FOR THERAPY
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US-09-338-933-5
                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 531
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                              Query Match
Best Local Similarity
Matches 264; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09215681A Patent No. 6528253
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
MUMBER OF SEQ ID NOS: 310
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                                                                                                              226 GGCGTCGATCAGCAAGGTGAACGTAATAGAACCATGGCTCAGTTTTCCCACACCTTTCGGT
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                                                     286 GGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAAGGGCCAAGCATGACCAGCAGTTC 345
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                    GGAGGGCCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTT
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ilarity 61.3%;
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Pred. No. 1.5e-29;
0; Mismatches 161;
                                                                                                                                                                            Score 151.4; DB 4;
Pred. No. 1.5e-29;
                                                                                                                                                            Mismatches 161;
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                                                                                                                                                            Indels
                                                                                                                                                                                           Length 531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 60, Application US/09404879A
PATENT NO. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REPERBNCE: 210121.462C2
CURRENT APPLICATION UNMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOPTWARDE: RESECTOR OF WITCHESS.
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SEQ ID NO 60
LENGTH: 480
TYPE: DNA
ORGANISM: Homo s
US-09-404-879A-60
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US-09-404-879A-60
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                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
247; Conserv
ATCATGAAACAACCCC-----
                                 GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT 618
                                                                                                                                                                                                                                    GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 438
                                                                                                                                                                                                                                                                                                                                                    ATGGCTCAGTTTCCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTGAA 73
                                                                                                                                                                                                                                                                                                                                                                                       ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG
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                                                                                                                                                                       GGTGATCAAGCCCGTACTTTTTCCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAA 193
                                                                                                                                                                                                                                                                                                                   GAAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FastSEQ for Windows Version
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llarity 62.1%;
Conservative
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Pred. No. 1.2e-27;
D; Mismatches 145
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RESULT 10
US-09-338-933-60
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CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 60
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APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
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Patent No. 652825
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                                                                                                                                                 GENERAL INFORMATION:
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                                                             APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF OVARIAN CANCER
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CURRENT APPLICATION NUMBER: US/09/215,681A CURRENT FILING DATE: 1998-12-17 NUMBER OF SEQ ID NOS: 310
                                                   FILE REFERENCE: 210121.463
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Pred. No. 1.2e-27;
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US-09-215-681-60
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Best Local Similarity
Matches 247; Conserv
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                                                                                          GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT 618
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Pred. No. 1.2e-27;
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RESULT 12 US-08-728-323A-1 Sequence 1, Application US/08728323A Patent No. 5948676 Patent No. APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Pattrick S.
TITLE OF INVENTION: Immediate Ea
TITLE OF INVENTION: Sarcoma-Asso
TITLE OF INVENTION: Encoding Sam GENERAL INFORMATION: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA: ATTORNEY/AGENT INFORMATION: NAME: White, John P. COMPUTER READABLE FORM: NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS: APPLICANT: NAME: White, John P. REGISTRATION NUMBER: APPLICATION NUMBER: FILING DATE: STATE: STREET: 1185 Av. CITY: New York CLASSIFICATION: 435 ZIP: COUNTRY: ADDRESSEE: 10036 New York 1185 Avenue of the Americas U.S.A. Bohenzky, Chang, Yuan Cooper & Dunham Encoding Same And Uses Thereof Sarcoma-Associated Herpesvirus, Immediate Early Protein From Kaposi's Roy US/08/728,323A 28,678 Version #1.30

2312 2597 2252 2537 2192 2477 2132 2417

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US-08-728-323A-1
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Best Local Similarity
Matches 534; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
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TYPE: nucleic acid
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Pred. No. 4e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 3489
TYPE: DNA
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APPLICANT: Kieff, Elliott D.

APPLICANT: Ballestas, Mary E.

APPLICANT: Kaye, Kenneth M.

TITLE OF INVENTION: FRADING VIRUS LANA ACTS IN TRANS ON

TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISO

FILE REFERENCE: 16412-10001R
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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RESULT 14

US-09-410-399-1

US-09-410-399-1

Sequence 1, Application US/09410399

Patent No. 6482587

GENERAL INFORMATION:

APPLICANT: Robertson, Erle S.

APPLICANT: Cotter, Murray A.

TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral

TITLE OF INVENTION: to Genomic Host DNA

FILE REFERENCE: UM-03778
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Matches 534; Conserv
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Pred. No. 4e-27;
0; Mismatches 650;
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Patent No. 5849564

Patent No. 5849564

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
APPLICANT: MOORE, PATRICK S.
TITLE OF INVENTION: POLYPEPTIDES FROM TITLE OF INVENTION: HERPESVIRUS, DN
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US-08-770-379-20/c
                                                                                                                                JS-08-770-379-20
                                                      Query Match
Best Local Similarity
Matches 534; Conserv
                                                                                                                                                                               TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/08770379 Patent No. 5849564
                                                                                                                                            STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patenti
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                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/770,379 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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1233 GGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAGCAGCAGGAGAAGAACT
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85 Avenue of the Americas
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                                                      Score 144; DB 2; I
Pred. No. 1.5e-26;
0; Mismatches 650;
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RESULT 1

US-09-884-441-72

Sequence 72, Application US/09884441

Patent No. US20020119158A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: ALGATE, Darrick

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C7

CURRENT APPLICATION NUMBER: US/09/884,441

CURRENT FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 489

SOFTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 72

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Sequence 311, App
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Sequence 5, Appli
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Sequence 19759, A
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Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 72, Appl Sequence 72, Appl Sequence 72, Appl Sequence 75, Appl Sequence 193, Appl Sequence 193, App Sequence 31258, App Sequence 31258, App Sequence 31, App Sequence 39, Appl Sequence 17127, A Sequence 30453, A Sequence 17146, A Sequence 103144, A

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RESULT 2
US-09-907-969-72
; Sequence 72, Application US/09907969
; Publication No. US2003009180A1
; GENERAL INFORMATION:
   APPLICANT: Mitcham, Jennifer L.
   APPLICANT: Mitcham, Jennifer L.
   APPLICANT: Ming, Gordon E.
   APPLICANT: Algate, Paul A.
   APPLICANT: Filing, Steven P.
   APPLICANT: Fanger, Gary Richard
   APPLICANT: Recter, Marc W.
   APPLICANT: Vedvick, Thomas S.
   APPLICANT: Carter, Darrick
   APPLICANT: Hill, Paul
   APPLICANT: HIL, Paul
   APPLICANT: Albone, Earl
   APPLICANT: HILL, Faul
   APPLICANT: HILL, Paul
   APPLICANT: HILL, Paul
   CURRENT FILING DATE: 2001-07-17
   NUMBER OF SEQ ID NOS: 596
   SOFTWARE: FastSEQ for Windows Version 4.0
   SEQ ID NO 72
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B & B & B	5 B 6 B	8 B 8	y b	S B S	Db Qy	Q B Q	Db Qy	р Оу	dg dg	d dy	QУ	ОУ
1842 GCTCTTGAAAAGAAACTGCATCTAAGCTCTCAGAAATGGATTCAGTTTAACAATCAGCTG 1901 2077 AAGGAACTGAAGAAACAATCAGCAACACCACCAGCAGCAGCAGCAGCAGCTCCATGAAAATCAGCTC 2136		1802 ACIGNOLINGANGITIIGGALAACAGIGIGACCIGGAAATITAIGGAAAICAACITI 1861 1837 CAGCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTTATTCCAGAGAACAACAGATA 1896		1657 ACCGTGGTCCTGAAGGCAAGGAGGAAGACTCTGGAGTTTGAGTTAGAAGCTCTGAATGAC 1716		1477 GAGCTGGAGAAGCAGCTGGAGAAGCAGCGGAGCTGGAGCGGCAGCGAGAGAGGAGAGAGG 1536	1417 CGCGCCGAGCAGGAGAGAAAAGAGCGGGAGGCCCAGGAGCAGGAGG	1357 CGCCGCCAAGCGCTCTTGGAGCAGCAGCAGCAAAAAAGCAGGAGCAGGATTGGCTCAGCTGGAG 1416	1297 GTGACATTTGAGGATANGAAGCGGGAGACTTCGAGCGAGGAGTGGGAGAGG 1356	1237 CAGAGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAGCGAGAGAAAACTGCCT 1296	1177 TCCTTCAGAAAAGTTCGCTCCGGCAGTGGGATGTCCGTCATAAGCTCTTCTTCTGTGGAT 1236	1117 GATGTTGCCAIGTCTGGTCAGCCACTGCCGCCCGCCCTCCAGAATACATCCCTCCT 1176

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Sequence 72, Application US/09827271

Publication No. US20030165504A1

GENERAL INFORMATION:
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C6

CURRENT APPLICATION UNUMBER: US/09/827,271

CURRENT FILING DATE: 2001-04-04

NUMBER OF SEQ ID NOS: 461

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 72

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Best Local Similarity 55.4%;
Matches 1128; Conservative
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ORGANISM: Homo sapien
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Pred. No. 1.1e-128;
0; Mismatches 812;
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Sequence 72, Application US/10198053

Publication No. US20030124140A1

GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Hill, Paul

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C9

CURRENT APPLICATION NUMBER: US/10/198,053

CURRENT FILING DATE: 2002-07-17

NUMBER OF SEQ ID NOS: 624

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 72

LENGTH: 2017

TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 568
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                          Matches
                                                                                                                                        Query Match
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                                                                                                                                                                                        LOCATION: (556)
OTHER INFORMATION: I
NAME/KEY: SITE
LOCATION: (562)
OTHER INFORMATION: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
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       ACCATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTG
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GENERAL INFORMATION:
                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version

CURRENT APPLICATION NUMBER: US/09/879,957

APPLICATION NUMBER: US/09/879,957
                                                                                                     FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                     APPLICATION NUMBER: US 0
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
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STATE: New York
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                                                                                                                                                                                                                                                                                                COUNTRY: USA
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INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
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KAY, Brian K.
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                                                                                                                                                                                                                                                                                                                                                Pennie & Edmonds LLP
55 Avenue of the Americas
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MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID
US-09-879-957-193
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Best Local Simi
Matches 633;
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 bases
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                    CAAAGGATCAAGAGAGTTTTTGGGAGTGCTAGCAAGTCTGGAGCATCAAATAAAAAACCTG
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 GTCCAAGTAGTGAAAGAGCCACACCTGCCTTTCATC--
                             AAGCTCGAGGGAAAAAGCGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCTAA
                                                                                                                           ACTGGTGGACGGGAACGGTGGGCGACAAGTCCGGAGTCTTCCCCTTCTAACTATGTGAGGC
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                                                              AGGCCAGAGGAAAAAAGCGACAGAAAGGATGGTTTCCTGCCAGTCATGTTAAACTTTTGG
                                                                                                                                                                                      AGATTGCTCAGGTAACTTCAGCATATGTTGCTTCTGGTTCTGAACAACTTAGCCTTGCAC
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Pred. No. 1.1e-84;
0; Mismatches 363;
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No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 125
LENGTH: 4210
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 125, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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CURRENT FILING DATE: 2001-01-17
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                                                                                                                      1215
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                                                                                                                                                                                                                     AGAAGGGTTGGTTCCCCCAAGTCTTACGTGAAACTCATTTCAGGGCCCCGTAAGGAAATCCA
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                                                                            CCGCCAAGCCAGCCATTCCCCGGAGAAGAGTTTATTGCCATGTACACATACGAGAGTTCTG
                                                                                                                                                        CAAGCATCGATACTGGCCCTACTGAAAGTCCTGCTAGTCTAAAGAGAGTGGCTTCCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGTCAGGTGATTGCTATGTATGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTCT
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ilarity 61.0%;
Conservative
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Pred. No. 4.9e-84;
0; Mismatches 361;
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AACCTGGAGATTTGACTTTCACAGAAGGTGAAGAAATATTGGTGACCCAGAAAGATGGAG

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; SEQ ID NO 31258
LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(503)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OB:
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILLNG DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILLNG DATE: 1999-01-20
PRIOR FILLNG DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-918-995-31258

; Sequence 31258, Application US/09918995

; Publication No. US20030073623A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                        Query Match
Best Local Similarity
                                                                         Matches
                                                                                                                                                09-918-995-31258
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                                 1081 ACTGCAGAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCA 1140
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   AATTCAGAGGAATTTATCCTGGCAATGCACCTCATTGATGTAGCTATGTCTGGCCAACCA
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                                                                       Score 322.6; DB 1
Pred. No. 3.7e-82;
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US-09-879-957-39
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Patent No. US200200347
GENERAL INFORMATION:
TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTER
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
KAY, Brian K.
FOWLKES, Dana M.
MCCONNELL, Stephen J.
MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOWALN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                        NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 790-999
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ADDRESSEE: Pennie &
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ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
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                                                                          TELEFAX: (212) 869-8864/9741
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LENGTH: 747 bases

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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DA
SEQUENCE DESCRIPTION: SEQ ID
US-09-879-957-39
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APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXOITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXOITILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION UNMER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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Best Local Sim:
Matches 418;
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                                                                                                                                                                                                         Sequence 17127, Application Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                               GTTATGAACAAAGATGATCCTGATTGGTGGCAAGGAGAGATCAACGGGGTGACTGGTCTC
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Pred. No. 2.4e-63;
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SEQ ID NO 17127
LENGTH: 270
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            Matches
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OTHER ING
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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FIER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 2.2

FHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

THER INFORMATION: EXPRESSED IN PLACENYRA, SIGNAL = 2.3

FHER INFORMATION: EXPRESSED IN PLACENYRA, SIGNAL = 2.3

FHER INFORMATION: EXPRESSED IN PLACENYRA, SIGNAL = 1.6

FHER INFORMATION: EXPRESSED IN HEATH AND SIGNAL = 1.8

FHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2

FHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

FHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

FHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7

FHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2

THER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2

FHER INFORMATION: SWISSPOT HIT: Q15811, EVALUE 1.00e-112

FHER INFORMATION: NT HIT: 9111526214, EVALUE 0.00e+00
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00666
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                        AAACCAGTGACCGATCTGACATCTGCCCCCTGCCCCCAAACTGGCTCTGCGTGAGACCCCT
                                                                                                                                                                                                             GTGGATGAAAGCCCAGACTGGAGAGCCAGGATGGCTTGGAGGAGAGCTGAAAGGGAAGACG
                                                                                                                  GGATGGTTCCCTGCAAACTATGCAGAAAAGATTCCAGAAAAATGAGGTTCCCACTCCAGCC
                                                                                                                                                                               GTGGATGAAAGCCAAACTGGAGAACCCGGCTGGCTTGGAGGAGAATTAAAAGGAAAGACA
                                                                                       GGGTGGTTCCCTGCAAACTATGCAGAGAAAATCCCCAGAAAATGAGGTTCCCGCTCCAGTG
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Pred. No. 1.6e-46;
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                                                    OTHER INFORMATION: NOTHER 
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                       LENGTH: 286
TYPE: DNA
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APPLICATION NUMBER: PCT/US01/00668
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     INFORMATION:
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Chen, Wensheng
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N: MAP TO APO00311.1

N: EXPRESSED IN BT474, SIGNAL = 0.87

N: EXPRESSED IN BOME MARROW, SIGNAL = 1.3

N: EXPRESSED IN HBL100, SIGNAL = 1.3

N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66

N: EXPRESSED IN LUNG, SIGNAL = 0.66

N: EXPRESSED IN BRAIN, SIGNAL = 0.69
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/0066
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                                                                                                                            APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00665
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NT HIT: AF114488. 1, EVALUE 0.00e+00
SWISSPROT HIT: Q15811, EVALUE 2.00e-45
EST_HUMAN HIT: AA773263.1, EVALUE 1.00e-112
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US-09-864-761-17146
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                               APPLICANT: Kank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT FILMG DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                  Sequence 17146, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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PRIOR FILING DATE: 2001-01-29
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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N: EXPRESSED IN LUNG, SIGNAL = 0.7

N: EXPRESSED IN HELA, SIGNAL = 2.4

N: EXPRESSED IN PLACENTA, SIGNAL = 1.2

N: EXPRESSED IN BT474, SIGNAL = 0.76

N: EXPRESSED IN BT474, SIGNAL = 1.3

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

ON: EXPRESSED IN ADULT LIVER, SIGNAL = 1

ON: EXPRESSED IN ADULT LIVER, SIGNAL = 0

ON: EXPRESSED IN GOME MARROW,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-01-30
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Pred. No. 1.7e-46;
0; Mismatches 32;
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LENGTH: 301
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ORGANISM: Homo
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00666
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APPLICATION NUMBER: US 09/608,408
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
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GCCGCCAAGCGCTCTTGGAGCAGCAGCGCCAAAGAGCAGCAGCGGTTGGCTCCAGCTGGAGC
                              GGGCGGAGCAGGAGGAAGGAAGGAGCGTGAGCGCCAGGAGCAAGAGCGCAAAAAGACAACTGG
                                                                                            GAAGGCAAGCTCTCCTGGAACAGCAGCGCGCAAGGAGCAGCAGCGCCCTGGCCCAGCTGGAGC
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N: EXPRESSED IN FETAL LIVER, SIGNAL = 3.0

N: EXPRESSED IN BRAIN, SIGNAL = 2.6

N: EXPRESSED IN BLACENTA, SIGNAL = 2.3

N: EXPRESSED IN BT474, SIGNAL = 2.2

N: EXPRESSED IN BONE MARROW, SIGNAL = 3.4

N: EXPRESSED IN HELA, SIGNAL = 3.7

N: EXPRESSED IN HELA, SIGNAL = 3.7

N: EXPRESSED IN LUNG, SIGNAL = 2.2

N: EXPRESSED IN LUNG, SIGNAL = 2.2

N: SWISSPROT HIT: O35601, EVALUE 3.50e-01

N: NITSPROT HIT: AF114487.1, EVALUE 3.50e-122
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EXPRESSED IN HBL10
EXPRESSED IN FETAL
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Pred. No. 2e-46;
0; Mismatches
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HBL100, SIGNAL = 3.2
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                                                                                                                                                                      SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 17644
LENCTH: 263
TYPE: DNA
                                                  PEATURE:
OTHER INFORMATION: MAP TO A
OTHER INFORMATION: EXPRESSE
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TITLE OF INVENTION: HUMAN GENOME-DERIVED
TITLE OF INVENTION: GENE EXPRESSION ANAL
FILE REFERENCE: Acomica-X-1
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NUMBER OF SEQ ID NOS: 49117
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CURRENT FILING DATE: 2001-05-23
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                                  OTHER
                                                                                                                                                        ORGANISM: Homo sapiens
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FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00664
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                   INFORMATION:
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Hanzel, David K.
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SSSED IN BONE MARROW, SIGNAL
SSSED IN ADULT LIVER, SIGNAL
ESSED IN BRAIN, SIGNAL = 4
SSSED IN PLACENTA, SIGNAL = 3
SSSED IN BT474, SIGNAL = 2.9
SSSED IN HBL100, SIGNAL = 2.9
SSSED IN LUNG, SIGNAL = 3.2
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US-09-864-761-10314
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PELING DATE: 2000-02-04
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-06-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: DOT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PRICING DATE: 2001-01-30
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                                                                       PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Penn, Sharron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Aeomica-X-1
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APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00662
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Chen, Wensheng
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EXPRESSED IN FETAL LIVER, SIGNAL = 5.3

EXPRESSED IN HEART, SIGNAL = 2.9

EST HUMAN HIT: BE542917.1, EVALUE 3.00e-62

SWISSPROT HIT: 035601, EVALUE 2.80e-01

NT HIT: AF114487.1, EVALUE 1.00e-122
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Best Local Similarity 81.6%;
Matches 222; Conservative
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 10314
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MAP TO APO00311.1

OTHER INFORMATION: EXPRESSED IN BY TO ARROW, SIGNAL = 0.87

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.66

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.69

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.69

OTHER INFORMATION: EXPRESSED IN PEACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.92

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION:
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
                                 2763 GCCCTCCACAACCCCCAACAACTGGGCAGACT 2794
                                                                                                                                      2703 CCCTGCCCCAAACTGGCTCTGCGTGAGACCCCTGCTCTTTGCCAGTGACCTCTTCTGA 2762
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                                                                                             CCCTGCCCCAAACTGGCCTTGCGTGAGACCCCCCGCCCCTTTGGCAGTAACCTCTTCAGA 448
GCCCTCCACGACCCCTAATAACTGGGCCGACT 480
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Search completed: December 5, 2003, 06:15:39 Job time: 1089.45 secs

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Perfect score:
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| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Human SH3D1A cDNA
Human SH3D1A cDNA
DNA encoding novel
Human SH3D1A cDNA.
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AAZ39009
ID AAZ3
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Human breast cell	ABA46803	22	270	5.5	198.8	5
v	ACA57579	25	701	5.7	206	*5
DNA encoding novel	AAS84759	23	395	5.8	210.8	ω
Human secreted exp	AAA44038	21	346	6.9	250	N
Human SH3P18 gene.	AAT39796	17	747	7.1	258	_
Human cDNA clone (AAH08146	22	676	7.1	260	0
Human cDNA clone (AAH03435	22	831	7.7	281	Θ
cDNA encoding nove	AAS27090	22	4210	9.1	331.4	œ
DNA encoding novel	ABK43586	23	3746	9.1	331.4	7
Human clone 65 gen	AAT39799	17	2873	9.1	٠	o
Human ovarian anti	ABQ55007	24	2067	9.4	٠	О
	ABK43814	23	568	9.8	356	4
cDNA encoding nov	AAS31621	22	568	•	356	ω
	AAI63919	22	568	•	356	Ņ
Human	AAI80000	22	548	9.8	ഗ	_
Human cDNA sequenc	AAH15260	22	1329	10.6	•	0
Ovarian carcinoma	ABN72656	24	2017	13.1	477.4	ø
Human ovarian carc	AAA69762	21	2017	13.1	477.4	æ
CDNA	AAK93179	22	877	13.3	485.4	7
cDNA 5'-er	AAK91610	22	877	13.3	485.4	o
Human adipocyte Se	ACA57641	25	677	14.1	513.8	O1
ncodin	AAS02055	22	4447	17.8	4	*2
Ese2 coding	AAZ39011	21	3593	18.3	666.6	ω
	AAZ39026	21	6014	18.6	677	N
Ese2L codi	AAZ39027	21	4975	18.6	677	_
Mouse Ese2 full le	AAZ39010	21	4625	٠	677	0
Human polynucleoti	AAK52332	22	6103	٠	713.8	ω
gic disease	AAL47247	24	5828	٠	721	œ
SH3P17 ger	AAT39795	17	1389	23.6	858	7
	AAK94611	22	1676	30.3		σ
SH3D:	AAZ34574	20	3231	34.4		տ
Human cDNA sequenc	AAH16578	22	2131	34.6	1259.2	*5
DNA encoding novel	AAS84762		2874	35.5	1291.4	ω
Human full-length	AAK94139	22	2131	. 40.7	1483.8	N
		20	2079	41.0	1495	_
	AAI63825	22	3466	56.1	2043.8	0
DNA encoding novel	ABK43498	23	3319	56.1	2043.8	Φ

ALIGNMENTS

AAZ39009 standard; cDNA; 3723 BP.

Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral; ss. WPI; 2000-052802/04 27-APR-1998; 05-FEB-1999; 04-NOV-1999. AAZ39009; Egan SE, 27-APR-1999; WO9955728-A2. de enw Mouse Esel coding sequence 28-FEB-2000 (first entry) (HSCR-) HSC RES & DEV LP. Wang W, Sengar A; 98CA-2230201 99US-0118739 99WO-CA00375.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antagonists of an Ese binding partner are used to treat diseases associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell cultures, while administration of (I) is used to promote endocytosis of selected cells. (Ant) agonists of (I) or Ab are used to suppress abnormal proliferation of cells that can be stimulated to proliferate by a growth factor receptor; and similar compounds (also inactive Ese mutants) can be used to prevent viral infection. Endocytosis may also be regulated, in vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding dynamin to the complex. Generally conditions that can be treated include cancer; abnormal cell division or migration; viral infection; or abnormal receptor signalling, tissue development or synaptic transmission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex with Espl5 protein), vesicular trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, mimetics, fragments and inactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with Esp15 protein, vesicular trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists, mimetics, fragments and inactimutants); (I)-specific antibodies (Ab); sequences antisense to the polynucleotide; agents that downregulate expression of Ese genes or
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                                      GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA
                                                        GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA
                                                                                                           GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAAC
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RESULT 2 AAZ39025 ID AAZ39025 standard; cDNA; 5144 BP. XX	2581 GACAACTGGGATACGTGGGCGGCTCAGCCTTCTCTGACCGTACCTAGTGCTGGCCAGTTA 2640	. da
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3481	2401 GAGGTTCCCACTCCAGCCAAACCAGTGACCGATCTGACATCTGCCCCTGCCCCCAAACTG 2460	g 6
3421	2341 GAGCTGAAAGGGAAGACGGGATGGTTCCCTGCAAACTATGCAGAAAAGATTCCAGAAAAT 2400	Qy Db
3361	2281 CCAGGAGATATAGTCATGGTGGATGAAAGCCAGACTGGAGAGCCAGATGGCTTGGAGGA 2340	Db 02
3301	2221 GTATATTACCGAGCGCTGTACCCCTTTGAATCCAGAAGTCACGATGAGATCACCATCCAG 2280	g <i>Q</i>
3 3 U	2161 CCCTGGTCTACCACAGAGAAAGGCCCGCTTACCATTTCTGCACAGGAGAGTGTAAAAGTG 2220	Db Qy
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2941	861 CAGAGGTCCCTGGAGGCAGCGCGACTGAAGCAGAAGAGAGAG	Qγ
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Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking;

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    Query Match
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  The present sequence encodes mouse Esel. The present invention specifically describes mammalian Esel and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex with Espl5 protein), vesicular trafficking and actin cytoskeleton.
                                                                                                                                                             Claim
                                                                                                                                                                                                                                 New nucleic acid encoding of endocytosis, used e.g.
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05-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; murine; Ese1; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse Esel full length cDNA sequence.
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CC generally (I) (or its (ant)agonists, mimetics, fragments and inactive cm thants); (I)-specific antibodies (Ab); sequences antisense to the (I) CC polynucleotide; agents that downregulate expression of Ese genes or ct antagonists of an Ese binding partner are used to treat diseases cC associated with undesirable endocytosis and resulting changes in cellular cC function. Particularly overexpression of Esel is used to block cC clathrin-mediated endocytosis in vivo or in cell cultures, while cC administration of (I) is used to promote endocytosis of selected cells. CC (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of CC cells that can be stimulated to proliferate by a growth factor receptor; CC and similar compounds (also inactive Ese mutants) can be used to prevent cultures, by forming an Ese-Espl5 complex, then binding dynamin to the CC complex. Generally conditions that can be treated include cancer; CC abnormal cell division or migration; viral infection; or abnormal cC receptor signalling, tissue development or synaptic transmission.
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Query Match Sequence 5082 BP; 1363 A; 1253 C; 1391 G; 99.7%; Score 3630; Pred. No. 0; 1075 贸 21; T; 0 other; Length 5082;

Local Similarity

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                                                                                                                                                                                                                                            SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy;
                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                     Human SH3D1A cDNA clone 11.
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CC involving the megakaryocytic lineage. The SH3DIA gene maps to the CS sequencing of 5 different sizes of CDNA clone from foetal brain CC (see AAZ34570-74) suggests that at least 3 isoforms exist. The CC invention provides methods for the diagnosis and treatment of CC megakaryocytic abnormality, myeloproliferative disorder, platelet disorder on chromosome 21. The CC megakaryocytic abnormality, myeloproliferative disorder, platelet conclusions and disorders, thromosocytopenia, CC platelet disorder on chromosome 21 low platelets in deletion for CC platelet disorder on chromosome 21 with leukaemias, neural conceptally, association of gains in chromosome 21 with leukaemias, neural conceptally, lissenceptally, and disorders including brain conceptally, lissenceptally, and colpoceptally. Methods are also CC microcephaly, lissenceptally, and colpoceptally. Methods are also CC provided for: suppressing cells unable to regulate thromour risk corresponded for a somatic alteration in the SH3DIA gene; monitoring CC microcepts or megakaryocytic abnormality, myeloproliferative disorder, consequence, platelet disorder or leukaemia; and colpocepts or megakaryocytic abnormality, myeloproliferative disorder, consequence, consequence, leukaemia or neural disorder using a concleic acid that expresses SH3DIA or its antisense nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of full-length cDNA (clone 11) corresponding to a novel human SH3 gene, termed the SH3DLA gene, that contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The SH3DLA gene maps to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid from the human SH3DIA gene and its products, useful the diagnosis and treatment of myeloproliferative disorders and
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  Sequence
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5195 BP; 1592 A; 1148 C; 1237 G; 1218 T;
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Ş 밁 á 밁 Ş 밁 S 밁 5 Matches Query Match Best Local Similarity 3167; 241 419 181 359 121 299 239 61 μ GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCCTCCACACTTCCCCCT GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180 GAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCAATATCTGGATTCATTACT ATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTAGAG ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG ATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGTGGAGTTTTCCATA GGTGATCAAGCTAGAAACTTTTTTTTTCAATCTGGGTTACCTCAACCTGTTTTAGCACAG Conservative 78.4**%**; 86.8**%**; 0 Score 2856; Pred. No. 0; Mismatches 475; DB 20; Indels Length 5195; ٠. و Gaps 240 298 300 478 418 358 120 60

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GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT

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GCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTCTGCACTTCCCCCT

2455 AAACTGGCTCTGCGTGAGACCCCTGCTCCTTTGCCAGTGACCTCTTTGTGAGCCCTCCACA 2514	QY Db	1378 AGGAACAAGGAGCAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAAGACTCTGGAGTTT 1437	~
	Qy dd	1318 CTGGAAAGGCAGCGACACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTGAATCAG 1377	J ~
	Ωγ	1258 CGGCAGCGAGAGGAGGAGGAGGAGGAGATCGAGAGGCGCGAGGCCCGAAAACGGGAA 1317 	5 ~
	dg Qy	1198 CAGGAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAG 1257	5 7
59	dg VQ	1138 GAGCGGTTGGCTCAGCTGGAGCGCGGCCGAGCAGGAGAGAGA	5 ~
	da	1078 GGCAGTGTGGAGCTGGAGAGCGCCCCCCCAAGCGCTCTTGGAGCAGCAGCAGCAGAAGAGCAG 1137	J .
	Db Q	1021 CCAGAGAAGAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGA 1077 	
	Ду	961 AGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAG 1020 	•
	Db	901 CCAGAATACATCCCTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGATGTCCGTCATA 960	•
	, pp 0	841 CTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCT 900	•
	D QY	781 TCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAAACTCACTGCAGAAGAATTTATC 840	5
	Db Qy	721 ACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCT 780	J \
	D Qy	661 TCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTATGAGTGGACACTTA 720 	• •
φω	Db Qy	601 GCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGAATGGGCTGTGCCTCAGTCA 660	0 \
29	da Ay	541 AAGAGTTCTTCCGTCCAGCAGATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAG 600 	•
	D 49	481 GGGGCTCCTCCCGTCATACAGCCTCTGCCTGCGTTTGCGCATCCTGCAGCCACATGGCCA 540	• •
3 9 8) D (421 GGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAAC 480	•
	D 44	361 GCTAGCATGCCACCACTCACAGCTGTTGCTGTGCCAATGGGCTCCATTCCAGTTGTT 420	
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AACAAGGAGGACCCGGACTGGTGGAAAAGGAGAAGTCAGTGGGCAAGTTGGGCTCTTCCCA
                                                                                    TACACCGCCCAGAACGATGACGAACTAGCCTTCAGCAAAGGCCAGATCATCAACGTCCTC
                                                                                                                                                                              ACTGAGCTACCCAAGACCGCAGTGCAGCCAGCAGTGTGCCAGGTGATCGGGATGTACGAT
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CC pathogenesis of leukaemias, both in general and in particular those convolving the megakaryocytic lineage. The SH3DIA gene maps to the CC involving the megakaryocytic lineage. The SH3DIA gene maps to the CC sequencing of 5 different sizes of CDNA clone from foetal brain CC (see AAZ34570-74) suggests that at least 3 isoforms exist. The CC invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet clisorder, acute leukaemia, neural disorders, thromobocytopenia, cC platelet disorder on chromosome 21, low platelets in deletion for C21, association of gains in chromosome 21 with leukaemias, neural CC abnormalities, dysfunctions and disorders including brain CC malformations and corresponding cognitive dysfunctions. CC microcephaly, lissencephaly, and colpocephaly. Methods are also CC provided for: suppressing cells unable to regulate themselves; CC progress or megakaryoctyic abnormality, myeloproliferative disorder, CC haematopoietic disorder, platelet disorder or leukaemia; and cc reatment of a subject (including a prenatal subject) having megakaryocytic abnormality, myeloproliferative disorder, platelet disorder using a collatelet disorder, leukaemia or neural disorder using a
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
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supplement; medical imaging; diagnostic; genetic disorder;
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC trestore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC diagnostic coding sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed cc at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity
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                                                                                                                                    CGGGGCTCCCCCTGTTATACAACCTCTGCCTGCATTTGCTCATCCTGCAGCCACATTGCC
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                                                              GATGACGAACTAGCCTTCAGCAA-AGGCCAGATCATCAACGTCCTCAACAAGGAGGAGCCC 3548
                                                                                                   AATTATGTCAAACTTCTAAGCCCCGGAACAAGCAAATCACCCCAACTGAGCTACCCAAG
                                                                                                                                                                                                                               AACAACTCACCCTGGCTCCTGGGCAGGCTGATTCTGATCCGGAAAAAGAA-CCCAGGTGGA
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GCTGACCACAGACAT-GGACCCCAGCCAGCAATG
                          TGACTGGTGGAAAGGAGAAGTCAATGGACAAGTGGGGCTCTTCCCATCCAATTATGTGAA
                                      GGACTGGTGGAAAGGAGAAGTCAGTGGGCAAGTTGGGCTCTTCCCATCCAATTATGTAAA 3608
                                                                                                                                                                                        TGGTGGGAAGGAGACTGCAAGCTCGAAGGAAAAAAGCGCCAGATAGGGTGGTTTCCAGCA 3369
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RESULT 8
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KW SH3D
KW mega
                                                                    AAZ34570
                                                                    standard; cDNA; 5199
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01-FEB-2000

entry)

Human SH3D1A CDNA.

SH3D1A gene; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder

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Best Local Sim
Matches 2960;
                                                                                                                                                                                                                                                                                                                                        dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissenceph and colpocephaly. Methods are also provided for: suppressing cells unable to regulate themselves; screening for a somatic alteration in the SH3DIA gene; monitoring the progress and adequacy of a treatment; monitoring tumour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, haematopoietic disorder, platelet disorder or leukaemia; and treatment of a subject (including a prenatal subject) having megakaryoctyic abnormality, myeloproliferative disorder, platelet disorder using a platelet disorder, leukaemia or neural disorder using a possible of the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at least 3 isoforms exist. The invention provides methods for t diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, neural disorders, thromobocytopenia, platelet disorder on chromosome 21; low platelets in deletion for 21, association of gains in chromosome 21 with leukaemias, neural abnormalities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  candidate region for low platelets on chromosome 21. Sequencing of 5 different sizes of cDNA clone (see AAZ34570-74) suggests that at least 3 isoforms exist. The invention provides methods for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the development of platelets and the pathogenesis of both in general and in particular those involving the megakaryocytic lineage. The SH3DIA gene maps to the sma
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haematopoietic disorder; cognitive dysfunction; microcephaly;
lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy;
                                                                                                                                                                                                                                                                                        Sequence
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The invention describes an isolated nucleic acid molecule (I) encoding a covel central nervous system protein. (I) and polypeptides (III) encoded (I) y(I), are used to treat a medical conditions and in diagnosis of a gathological condition. Disorders which are diagnosed or treated include (I) antological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative (I) disorders e.g. neoplasms of the breast or liver, cardiovascular disorders (I) cardiac arrest, cerebrovascular disorders e.g. cardiovascular disorders (I) anylotrophic lateral sclerosis, infections caused by bacteria, viruses (I) anylotrophic lateral sclerosis, infections caused by bacteria, viruses (I) acquired immunodeficiency virus (AIDS) and fungi, ocular disorders (I) adenocarcinomas and irritable bowel syndrome, reproductive system (I) adenocarcinomas and irritable bowel syndrome, reproductive system (I) disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes (I) and pituitary dwarfism, cancers and disorders at the cellular level e.g. (I) respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cacute kidney failure and blood related disorders e.g. myocardial (I) infarction. The polypeptides can also be used to aid wound healing and (I) infarction. The polypeptides can also be used to aid wound healing and (I) contrease or decrease storage capabilities, fat content, lipid, protein, to correase or decrease storage capabilities, fat content, lipid, protein,
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                                                            CCCGTCCTGCCTCCAGAATACATCCCTCCTTCCAGAAGAGTTCGCTCCGGCAGTGGG
                                                                                                           GAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCG 888
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ATATCTGTCATAAGCTCAACATCTGTAGATCAGAGGCTACCAGAGGAACCAGTTTTAGAA
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  GCCAAGCCGGAAATGCAAGACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGCT
                                                                      CGAAAGATCATAGAATTAGAAAAAACAAAAAGAAGACCCAAAAGACGAGCTCAGGAAAGG
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                                          CACGAAGAGGAAAAACTGAAAAAGGGAGGAGGAGTGTCAAAAAGAAGGATGGCGAGGAAAAA
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                       TCCCCATCTCCCGTCCTGGGCCAGGGTGA
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AAI63825 standard; CDNA; 3466

(first entry)

Human polynucleotide SEQ ID NO 33.

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RESULT 10
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AC Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cyrostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; ss. 31-JAN-2000; 2000US-0179065 04-FEB-2000; 2000US-0180628 24-FEB-2000; 2000US-0184664 17-JAN-2001; WO200155308-A2 2001WO-US01309

2000US-0186350. 2000US-0189874. 2000US-0190076. 2000US-0198123. 2000US-0205515. 2000US-0209467.

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                                                     WPI; 2001-488781/53.
P-PSDB; AAM43519.
        Claim 1;
                         New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders -
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2000US-0236370.
2000US-0237038.
2000US-0237039.

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CC The invention relates to human polynucleotides (AAI63803-AAI64012) and CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating CC or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the CC specification. The nucleic acids, proteins, antibodies and (ant)agonists CC are useful in the diagnosis, treatment and prevention of: (a) cancer, CC e.g. breast and ovarian cancer and other cancers of the adramal gland, CC companital, (b) immune disorders e.g. Addison's disease, allergies, CC autoimmune hammolytic anaemia, autoimmune thyroiditis, diabetes mellitus, CC crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC colitis, (c) cardiovascular disorders such as myocardial ischaemias, CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC core. The semence data for this natural did not form part of the
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Matches 2324;
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CC This is the nucleotide sequence of a cDNA clone, termed clone 5, CC corresponding to a novel human SH3 gene, termed the SH3DIA gene, CC that contributes to the development of platelets and the SH3DIA gene, CC involving the megakaryocytic lineage. The SH3DIA gene maps to the CC involving the megakaryocytic lineage. The SH3DIA gene maps to the CC sequencing of 5 different sizes of cDNA clone from footal brain CC (see AAZ34570-74) suggests that at least 3 isoforms exist. The CC invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet CC invention concerns and corresponding on thromosome 21.

CC platelet disorder on chromosome 21 low platelets in deletion for CC 21, association of gains in chromosome 21 with leukaemias, neural CC abnormalities, dysfunctions and disorders including brain CC microcephaly, lissencephaly, and colpocephaly. Methods are also CC provided for: suppressing cells unable to regulate themselves; CC microcephaly, lissencephaly, and colpocephaly, methods are also CC progress or megakaryoctyic abnormality, myeloproliferative disorder, chaematopoietic disorder, platelet disorder or leukaemia; and CC treatment of a subject (including a prenatal subject) having CC megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, chaematopoietic acid that expresses SH3DIA or its antisense nucleic acid. CC nucleic acid that expresses SH3DIA or its antisense nucleic acid.
Query Match
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standard; cDNA; 2131 ВP

(first entry)

Human full-length cDNA, SEQ ID NO: 2646

cDNA; cDNA synthesis; oligo-capping; 88

07-JUL-2000; 2000EP-0114089.

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Best Local Similarity 86.0
Matches 1657; Conservative
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Best Local (
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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su A, Sugiyama T, Nagai
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostice as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating
                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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supplement; medical imaging; diagnostic; genetic disorder; ss.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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CC sequence and an oligonucleotide comprising a sequence complementary to a coligonucleotide which comprises a 3'-end sequence complementary to a coligonucleotide which comprises a 3'-end sequence complementary to a coligonucleotide which comprises a 3'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in coliform the primer sets can be used in antisense therapy and coliform the primers are useful for synthesising polynucleotides, coliform and/or diagnosis of the primers are also useful for the collection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification cc of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3D1A gene;
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haematopoietic disorder, platelet disorder or leukaemia; and
treatment of a subject (including a prenatal subject) having
megakaryocytic abnormality, myeloproliferative disorder,
platelet disorder, leukaemia or neural disorder using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3231 BP; 1004 A; 721 C; 712 G; 794 T; 0 other;
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                               GCTGAAAGGGAAGACGGGATGGTTCCCCTGCAAACTATGCAGAAAAGATTCCAGAAAATGA
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                                                                                                                                  GTATTACCGGCACTGTACCCCTTTGAATCCAGAAGCCATGATGAAATCACTATCCAGCC
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ATTAAAAGGAAAGACAGGGTGGTTCCCTGCAAACTATGCAGAGAAAATCCCCAGAAAATGA
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Pred. No. 3.7e-289;
0; Mismatches 272; Indels
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*	CGC 3482	423 ACCCAAGACCGCAGTGCAGCCAGCAGTGTGCCAGGTGATCGGGATGTACGATTACAC 	
	3422 3CC 1707	3363 TCCAGCAAATTATGTCAAACTTCTAAGCCCCGGAACAAGCAAAATCACCCCAACTGAG	
	HTT 3362	3303 AGGTGGATGGTAGGAAGAGCAGCTGCAAGGTAGAAAAAGCGCCAGATAGGGTGG 	
	2CC 3302 CC 1587	3243 TGGTCCCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTGATCCGGAAAAAGAAC 	
	TAC 3242	RGAAATTGCCCAGGTTATTGCTTCCTACGCTGC -GAAATTGCCCAGGTTATTGCCTCATACACCGG	
	1492	493	
	3AA 3182	3123 AGTCTTCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGCTGGG	
,	1492	1493	
	CGG 3122	3063 GATTGTGGTTACCAAGAAGATGGTGACTGGTGGACGGGAACGGTGGGCGACAAGTCC	
	1492	493	
	GT 3062	3003 TGCCATGTACACATACGAGAGTTCTGAGCAAGGAGATTTAACCTTTCAGCAAGGGGAI	
	1492	441	
	TAT 3002	943	
	rgC 2942 	2883 CATTTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCTG	
	CT 2882	AGAAGGGTTGGTTCCCCAAGTCTTACGTGAAA 	
	CAT 2822	763 AGACAACCACTTAAATTTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCCAAGAC 	
	2 / 6 Z	201 CCAGGGTGAAAAGGTGGAGGGGGCTACAAGCCCTATATCCTTGGAG	
	120	141 GCAGAGGTCGAAAAGCTTGGAACGCGCACGGCCACTGGCTCTCCTCCCCCGTCTCCTGTG	
	3GG 2702	CAGAGATCAGCCTTTACCCCAGCCACAGCCACTGGCTCCTCCCCATCT	
	ACG 2642 AG 1140	2583 CAACTGGGATACGTGGGCGGCTCAGCCTTCTCTGACCGTACCTAGTGCTGGCCAGTTACG	
	3GA 2582 3GA 1080	2523 CAACTGGGCAGACTTCAGTTCCACGTGGCCCAGCAGCTCAAACGAAAGCCAGAAACGGA	
	CTAA 2522	463 TCTGCGTGAGACCCCTGCTCTTTGCCAGTGACCTCTTCTGAGCCCTCCACAACCC	
•	3GC 2462 	403 GGTTCCCACTCCAGCCAAACCAGTGACCGATCTGACATCTGCCCC	

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TCAACGTCCTCAACAAGGA 35	3483 CCAGAACGATGACGAACTAGCCTTCAGCAAAGGCCAGATCATCAACGTCCTCAACAAGGA 3542	3483 1768 3543 3543 3603	\$ \$ \$ \$ \$ \$ \$
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Search completed: December 4, 2003, 15:50:26 Job time: 608.079 secs

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ALIGNMENTS

REFERENCE AUTHORS SOURCE ORGANISM RESULT 1 BC013578 COMMENT KEYWORDS VERSION ACCESSION DEFINITION Snoor TITLE REMARK JOURNAL NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305 Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer General Cancer Gene Homo sapiens, Similar to intersectin 1 (SH3 domain protein), clone IMAGE:3878242, mRNA.
BC013578
BC013578.1 GI:15488896 Direct Submission Strausberg, R. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2079) Homo sapiens BC013578 Homo sapiens (human) 20,79 bp mRNA linear HTC 04-MAR-2003

1496.6 1495 809.8 795.6

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BC013578 BC020269 CA324450 BQ942708

BC013578 Homo sapi BC020269 Homo sapi CA324450 UI-M-FY0-BQ942708 AGENCOURT

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Contact:
Dickson, N
R. M.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796
This clone has the following problem: retained intron.
Location/Qualifiers
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/tissue type="Lung, large cell c./clone_Tib="NIH MGC_68"
/clone_Tib="NHH MGC_68"
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/note="Vector: pCMV-SPORT6"
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mol_type="mRNA"

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(Dickson, Mark) mcd@paxil.stanford.edu
1., Schmutz, J., Grimwood, J., Rodriquez,
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504796
This clone has the following problem: no cloning site /
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven Jones, Jennifer Asano, Tan Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
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Homo sapiens, clone IMAGE:4899011,
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 2126)
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                                                                        /note="Vector: pOTB7"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                            tissue type="Pancreas, /clone_lib="NIH_MGC_42" /lab_host="DH10B-R" /
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                                C---CAGAGAAGAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGA 1077
                                                                        AGCTCAACATCTGTAGATCAGAGGCTACCAGAGGAACCAGTTTTAGAAGATGAACAACAA
                                                                                                            AGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAG
                                                                                                                                                  CCAGAATACATTCCACCTTCTTTAGAAGAGTTCGATCTGGCAGTGGTATATCTGTCATA
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UI-M-FY0-ccl-a-05-0-UI.rl NIH_BMAP_FY0 Mus
IMAGE: 6820974 5', mRNA sequence.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                               CA324450
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AUTHORS
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Query Match
Best Local Similarity
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1 (bases 1 to 818)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: pYX-5
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The following repetitive elements were
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                                                                                                                                                                                                                                                                               ATGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCAGAG
                                                                                                                      GATGAGCAGCAGCAGAGAAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAAC
                                                                                                                                                            GATGAGCAGCAGCAGAGAAAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAAC
TTCGAGCGAGGCAGTGTGGAGCTGGAGAGCGCCGCCAAGCGCTCTTGGAGCAGCAGCGC
                                  TTCGAGCGAGGCAGTGTGGAGCTGGAGAAGCGCCCCAAGCGCTCTTGGAGCAGCAGCAGCGC 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="whole brain"
//dev stage="embryo 13.5,14.5,16.5,17.5dpc"
//lab_host="PH108 (T1 phage resistant)"
//clone lib="NIH BMAP FYO"
//clone lib="NIH BMAP FYO"
//note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library teg
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
127 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6"
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BQ942708
BQ942708.1 GI:223:
EST.
Mus musculus (house
                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution informati
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                             Plate: LLAM13743 row: n column: High quality sequence start: 10
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Location/Qualifiers
 /lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_129"
/note="Organ: olfactory epithelium;
                                      /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6314690"
                                                                            organism="Mus
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ACCCACTT :
                                       AGAGGGCAAGAATTGAGAGCACGAAACAAGTCTAAAGGAGCTAAAAATTGCTTGAAATC
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TGACAAAAAGCATCAGCTAGAAGGAAAACTTCCGGATATCAGGTGGTCCACTGGCAACCC
                                      TGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGGT-GTCGACTGGCAACCC
                                                                          GCCACCCGTGGTCCTGAAAGCAAGGAGGAAGACTCTGGAGTTTGAGTTACAAGCTCTGAA
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Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                Group Phase
                                                                                                                The FANTOM Consortium ar 
Group Phase I & II Team.
                                                                                                                                                                                                                                                                                                Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                and Hayashizaki,Y.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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2890 GGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCTGCTAGTCTA 2949

Matches Best Local Query Match

750;

Conservative

<u>.</u>

Mismatches

Similarity

20.6%;

Score 748.8; DB 11; Pred. No. 1.8e-157;

Length

0;

Gaps

0

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URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Division of Experimental Animal Research in Riken contributed to
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TGSLGKKPBIAQVIASYAATGPEQLTLAPGQLILIRKKNPGGWREGELQARGKKRQIG
WFPANYVKLLSPGTSKITPTELPKTNAVPAVCQVIGMYDYTAQNDDELAPSKGQIINV
LNKEDPDWWKGEVSGQVGLFSSNYVKLTDMDPSQQWCSDLHLLDMLTPTERKRQYI
HELIVTESNYVNDLQLVTBIFQXPLTSSELLTBKEVAMIFVNWKELIMCNIKLLKALR
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RLAMDPRCKGMPLSSFILKPMGRVTRXPLIIXNILENTPENHPDHALKHALLEKAEEL
CSQVNEGVREKENSDRLEWIQAHVQCEGLSEQLVFNSVTNCLGPRKFLHSGKLYKAKS
NKELYGFLFNDFLLLTQITKPLGSSGTDKVFSPKSNLQYMYKTFIFLNEVLVKLPTD
PSGDEPIFHISHIDRVYTLAAESINERTAWQOKIKAASELYIFTSKKKRBKAYLVRSQ
RATGIGRLMYNVVEGIELKPCKSHGKSNPYCEVTMGSQCHITKTIQDTLNPKWNSNCQ
FFIRDLEQSYLCITVEERDQLSADDFLGRTEIRVADIKKDQGSKGPVTKCLLLHEVPT
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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protein 1A) (MGD|MGI:1338069, GB|NM_010587, evidence:
BLASTN, 99%, match=2267)
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/db_xref="GI:26349813"
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/strain="C57BL/6J"
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                                                                                                                                                                                                       EST.
Mus musculus
Mus musculus
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University oc
cDNA Library Arrayed by: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                      732 bp
UI-M-FY0-cde-p-10-0-UI.r1 NIH_BMA
IMAGE: 6832091 5', mRNA sequence.
                                                                                                                                                                                                                                                IMAGE: 6832091 5', mRNA
CA750495
CA750495.1 GI:25575732
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 732)
                                                                                                      Contact: Robert Strausberg,
                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                        Unpublished
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This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

The following repetitive elements were found in this cDNA sequence: 637-722. cCAG) m#Simple_repeat Seq primer: pyx-5.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Mol_type="manna"
/strain="C57BL/6"
/db_xref="manna"
/strain="C57BL/6"
/clone="linkAE; 6832091"
/clone="linkAE; 6832091"
/lab_host="bH10B (T1 phage resistant)"
/clone=lib="Null BMAP FY0"
/clone=lib=
```

AUGIN

Query Match

20.0%; Score 727.2; DB 14; Length 732;
Best Local Similarity 99.6%; Pred. No. 7.8e-153;
Matches 729; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ATGAGCAGCAGCCAGAGAAAGAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAGAACT CTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAG GTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGG CCACATGGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTA TGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAĞGCTGCCTGAGGGAGCCGTCGTCAGAGG AAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGC GTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCAGG TGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTATGA AGTTACAGAAGGCACAATCATTCGATGTCGCCAGCGCCCCCCCAGCAGCAGCAGAATGGGCTG AGTTACAGAAGGCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGCAGAATGGGCTG CCACATTGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACACTA CCGTCCTGCCTCCAGAATACATCCCTCCTTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGA CTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAACTCACTGCAG TGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTATGA 1069 480 1009 420 180 360 889 829 240 709 120 60 300 649

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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB248849 725 bp mRNA
UI-M-EXO-byj-m-24-0-UI.rl NIH_BMAP_EXO Mus
IMAGE: 5719103 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (house mouse)
                                                 /dev_stage="embryo 15.5 dpc"

//lab host="DH108 (TI phage resistant)"

//clome lib="NIH BMAP EXO"

//clome lib="NIH BMAP EXO"

//clome lib="NIH BMAP EXO"

//clome lib="NIH BMAP EXO"

//clome library was constructed according to Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                       /clone="IMAGE: 5719103"
/tissue_type="whole brain"
                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6"
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                            GGATGTGATTGTGGTTACCAAGAAAGATGGTGACTGGTGGACGGGAACGGTGGGCGACAA
TGGGAAAACAGGGAGTTTAGGAAAAAAACCTGAAATTGCCCAGGTTATTGCTTCCTACGC 3236
                                                                        GTCCGGAGTCTTCCCCTTCTAACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGC
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/dev stage="wmbole brain"
/dev stage="wmbryo 18.5 dpc"
/lab_nost="MIDB (TI phage resistant)"
/clone_lib="NIH_BMAP_EHOp"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed_according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
, is CAGCCACGAC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."
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Pred. No. 7.6e-152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 738)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                       Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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/organism="Mus musculus"
/mol type="mRNA"
/mol type="mRNA"
/strain="C57BL/6"
/db_xref="C57BL/6"
/db_xref="C47BL/6"
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/dev stage="embryo 18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EH0p"
/clone_lib="NIH_BMAP_EH0p"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed_according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone was contributed by the Brain Molecular Anatomy Project
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Matches 719; Conserv
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Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
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BU704308
BU704308.1 GI:23632308
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National Institutes of Health, Mammalian
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1 (bases 1 to 729)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                       TCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAACGGGGCTCCTCCCCGTCATACAG 501
                                                                                                                                                                                                                                                                                      GCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTTGGAATGTCTCCACCCTTAGTA
                                               TCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAGGCACAATCATTCGATGTCGCC 621
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                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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/dev stage="embryo 12.5dpc"
/lab_host="DH108 (TI phage resistant)"
/clone lib="NIH BMAP FOO"
/clone lib="NIH BMAP FOO"
/clone lib="NIH BMAP FOO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/clone lib="NIH BMAP FOO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: BcoR I;
/note="Organ: Brain; Vector: pYX- Asc; Vector: Brain and the clun was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX- Asc vector: The library tag sequence located between the Not I site and the polyA tail is TGAGAGAGCC. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 program coordinator.
206 c 174 g
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Pred. No. 8.6e-148;
0; Mismatches 3;
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                                                                                                                                                Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                CB521237
CB521237.1 GI:29354592
EST.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                          CB521237 706 bp mRNJ
UI-M-GHO-cem-g-10-0-UI.rl NIH_BMAP_GHO
IMAGE: 6841475 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 706)
                                                                                               sequence: 220-337, > (GGA)n#Simple_repeat
Seq primer: pYX-5.
                                                                                                                                                                                                                                                                      Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                           The following repetitive elements were found in this cDNF
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6841475"
                                                                                  Location/Qualifiers
                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                      Ph.D.
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  ATGCTTGGAAGACTTATTCCAGAGAAACAGATACTCAGTGACCAGT
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/tissue_type="Whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="PH108 (TI phage resistant)"
/clone_lib="NIH_BMAP_GH0"
/clone_lib="NIH_BMAP_GH0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
/note="Torgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
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/note="Torgan: Brain; Vector: pYX- Asc; Site_1: BcoR I;
/note="Torgan: Brain; Vector: pXX- Asc; Site_1: EcoR I;
/note="Torgan: Brain; Vector: pXX- Asc primed with oligo-dT grimer containing a Not I site. Double strand cpNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Query Match Best Local Similarity 1006 GAGGATGAGCAGCCAGAGAAAACTGCCTGTGACATTTGAAGATAAGAAGCGGGAG 1066 AACTTCGAGCGAGGCAGTGTGGAGCTGGAGAGCGCCGCCAAGCGCTCTTGGAGCAGCAG 1 GGGATGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCTGCCTGAGGAGCCGTCGTCA ATGCTTGGAAGACTTATTCCAGAGAAACAGATACTCAGTGACCAGT 1651 AGAGAGCTAAGAATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCAA 1609 CAGGATATCAGGTGTCGACTGGCAACCCAGAGGCAAGAAATTGAGAGCACGAACAAGTCT ACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAAGGAAAACTT CTCCTGAATCAGAGGAACAAGGAGCAGGAGGCACCGTGGTCCTGAAGGCAAGGAGGAAG CTCCTGAATCAGAGGAACAAGGAGCAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAAG GCAAAACGGGAACTGGAAAGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGAA GCAAAACGGGAACTGGAAAGGCAGCGACAACTTGAATGGGAACGGAACCGGAGACAGGAA CGGGAGCTGGAGCGAGAGGAGGAGGAGGAGGAAGGAGGATCGAGAGGCGCGAGGCC GAGCGCCAGGAGCAGCGCAAGCGGCAGCTGGAGCAGCAGCAGCTGGAGAAGCAG GAGCGCCAGGAGCAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAG CGCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGCCGGAGCAGGAGAGGAAAAGAGCGG AACTTCGAGCGAGGCAGTGTGGAGCTGGAGAAGCGCCGCCAAGCGCTCTTGGAGCAGCAG CAGGATATCAGGTGTCGACTGGCAACCCAGAGGCAAGAATTGAGAGCACGAACAAGTCT Conservative 19.3%; <u>,</u> Score 701.8; DB Pred. No. 4e-147; Mismatches 14; ω •• Indels Length <u>.</u>. Gaps 1545 1485 1425 1365 1185 1125 1065 1005 660 480 420 360 1305 1245 60 600 540 300 240 180 120 0

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REFERENCE
AUTHORS
TITLE
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Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 703)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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CB527154.1 GI:29360627
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This clone was contributed by the Brain Molecula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                     GAGGTGGAGAGAGAGCCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTG
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//lab_host="PHH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FYO"
/clone_lib="NIH_BMAP_FYO"
/note="forgan: Brain; Vector: pYX- Asc; Site 1: EcoR I;
/note="forgan: Brain; Vector: pYX- Asc; Site 1: EcoR I;
/note="forgan: Brain; Vector: pYX- Asc; Site 1: EcoR I;
/note="forgan: Brain; Vector: pYX- Asc; Site 1: EcoR I;
/note="forgan: Brain; Vector: pYX- Asc; Site 1: EcoR I;
/note="forgan: Brain; Vector: pYX- Asc; Site 1: EcoR I;
/note="forgan: Brain; Vector: pYX- Asc; Site 1: EcoR I;
/note="forgan: Brain; Vector: pYX- Asc; Site 1: EcoR I;
/note="forgan: Brain; Vector: Brain; 
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/tissue_type="whole brain"
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/strain="C57BL/6"
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UI-M-FY0-cdc-j-23-0-UI.rl NIH_BMAP_FY0
IMAGE: 6827736 5', mRNA sequence.
                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 713)
NIH-MGC http://mgc.nci.nih.gov/.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                              National Institutes of Health, Mammalian
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                                                                                     sequence: 341-458,
                                                                                                   The following repetitive elements were
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                                                                   primer: pYX-5
                                                                                                                                       clone was contributed by the
organism="Mus musculus"
/mol_type="mRNA"
                                                 Location/Qualifiers
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Matches 704;
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                                                                                                                     GACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAAACT 1484
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/clone="IMAGE: 6827736"
/tissue_type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="PHH10B (T1 phage resistant)"
/clone_lib="NHI_BMAP_FY0"
/note="Torgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

99 a 157 c 245 g 106 t 6 others
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Pred. No. 9.9e-145;
0; Mismatches 9;
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BASE COUNT

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REFERENCE
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Best Local Similarity
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                                                                                                                                                                                  686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB244555

UI-M-FY0-cdr-a-13-0-UI.rl NIH_BMAP_FY0 Mus musculus IMAGE: 6833270 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The following repetitive elements were found in this cDNA sequence: 413-530, >(GGA)n#Simple_repeat Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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TGGAAAACTCACTGCAGAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTC
                                                                                                              ATCAAGTTTACCCCAGGCTCAGCTGGCTTCAATATGGAAATCTTTCTGACATTGATCAAGA
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//dev stage="mbryo 13 5,14.5,16.5,17.5dpc"
//lab_host="DH10B (TI phage resistant)"
//clone_lib="NIH_BMAP_FYO"
//clone_lib="NIH_BMAP_FYO"
//note="Corgan: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the NotI site and the polyA tail
is ACCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

88 a 156 c 235 g 109 t
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/mol_type="mRNA"
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tissue_type="whole brain"
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99.7%;
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Pred. No. 2.7e-143;
0; Mismatches 2;
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RESULT 15
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                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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BQ719508.1 GI:21858405
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IMAGE:6188111 5', mRNA sequence.
BQ719508
                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13583 row: c column: 24
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National Institutes of Health, M
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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organism="Homo sapiens"
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/clone="IMAGE:6188111"
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Result
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1: /cgn2_6/ptodata/2

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10162.293 Million cell updates/sec
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US-09-404-879A-60
US-09-318-933-6
US-09-215-681-5
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US-09-215-681-4
US-09-249-585A-2
US-09-249-585A-2
US-09-338-933-3
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US-09-359-081-2
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Sequence 193, App
Sequence 39, Appl
Sequence 60, Appl
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LENGTH: 2017
TYPE: DNA
ORGANISM: Homo sapien
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APPLICANT: King, Gordon B.
APPLICANT: King, Gordon B.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
TILLE REFERENCE: 210121.462C2
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 1, Appli	Sequence 3, Appli	Patent No. 5273901	Sequence 209, App	Sequence 209, App	Sequence 3, Appli	Sequence 208, App	Sequence 208, App	Sequence 14, Appl		Sequence 15, Appl	-	Sequence 15, Appl	•	Sequence 15, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 14, Appl

ALIGNMENTS

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                                            342 ATCATGAAACAACCCCCTATGTTCTCTCCACTAATCTCTGCTCGTTTTTGGGATGGGAAGC
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                                                                                       GTCATGAAACAGCAACCAGTG----GCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGG
                                                                                                                                                                   GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT
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AATCAGAGGAACAAGGAGGAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAAGACTCTG
                                                                       CGGGAACTGGAAAGGCAGCACAACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTG 1371
                                                                                                                                              CTGGAGCGGCAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGCGCGGAAAA 1311
                                                                                                                                                                                      GAGCAGGAGCGGTTGGCTCAGCTGGAGCGCGCCGAGCAGGAGAGGAAAGAGCGGGAGCGC 1191
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                                                                                                                      GAGGCTGAACGCAAAGCCCAGAAAGAGAAGAAGAGTGGGAAGCGGAAAACAGAGAAACTG 1274
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GGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA
                                                                         GAAAGGGCCAAGCATTAGAGCTTAGCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT
                                                    GAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGGAGGTTACATAACA
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APPLICANT: Witcham, Jennifer Lynn
APPLICANT: King, Gordon E.
FITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.46201
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
SEQ ID NO 72
LENGTH: 2017
TYPE: DNA
ORGANISM: Homo sapien
US-09-338-933-72
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-09-338-933-72
; Sequence 72, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
                                                                         Query Match
Best Local Similarity
ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG
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ilarity 55.5%;
Conservative
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                       Sequence 72, Application US/09215681A
Patent No. 6538253
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: OF OVARIAN CANCER FILE REFERENCE: 210121.463
CURRENT APPLICATION MUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FRASESEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 2017
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                       GTCCTGCCTCCAGAATACATCCCTCCTTCCTTCAGAAGAGTTCGCTCCGGCAGTGGGATG
                                                  GAATTTATTCTGGCGATGCACCTCACTGACATGGCCAAAGCTGGACAGCCACTACCACTG
                                                                 GAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCCGCCC
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Best Local Similarity
Matches 631; Conserv
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APPLICANT:
APPLICANT:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 18,872
REFERENCE/OOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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                                                                                        GAAGAGGATGGTTTCCCAAATCTTATGTCAAGATCATTCCTGGGAGTGAAGTAAAACGGG 837
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KAY, Brian K.
FOWLKES, Dana M.
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VENTION: POLYPEPTIDES HAVING A FUNCTIONAL
VENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING
VENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                      SPARKS, Andrew B.
HOFFMAN, No. 6309820h
KAY, Brian K.
FOWLKES, Dana M.
POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME
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GENERAL INFORMATION:
GENERAL INFORMAN, No. 6309820h
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 63.9%;
Matches 418; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/630,915A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1:
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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                                     GTCCTCAACAAGGAGGACCCGGACTGGTGGAAAGGAAGTCAGTGGGCAAGTTGGGCTC
                                                                                                                                                 TATGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTCTCCAAGGGACAACTCATTAAT
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                                                                        GTTATGAACAAAGATGATCCTGATTGGTGGCAAGGAGAGCACACGGGGGTGACTGGTCTC
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Pred. No. 7.6e-55;
0; Mismatches 215; Indels
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RESULT 6 US-09-404-879A-60

Query Match

4.0%;

Score 144;

DB

4;

Length 480

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GENERAL INFORMATION:
APPLICANT: Witcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO
TITLE OF INVENTION: OVARIAN
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 60
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-60
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US-09-338-933-60
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US-09-338-933-60
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CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60, Application US/09404879A
Patent No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.46202
                                                                                                                                                                                                                                                                                     Sequence 60, Application US/09338933
Patent No. 6488931
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Best Local Similarity
             LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapien
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Pred. No. 1.9e-26;
0; Mismatches 145;
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Fundakis, Tony N.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
CURRENT FILIGATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FRSESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60, App. Patent No. 65282
                                                                                                                                                                                                                                                         Best Local Sim
Matches 247;
                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 60
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                                                                                                                                                                                                                                                                                                                                    LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapien
   194
                               181
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                                                                                                                          GAACGTACTAAGCATGATAAACAGTTTGATAACCTTCAAAACCTTCAGGAGGTTACATAACA
                                                                                                                                                        GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACT 120
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                            GGAAGCATGCCCAATCTGTCCATTCATCAGCCATTGCC
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ATATGGGCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATA
                                                            GGTGATCAAGCCCGTACTTTTTCCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09215681A
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                      4.0%;
62.1%;
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US-09-338-933-5

Sequence 5, Application Patent No. 6488931 GENERAL INFORMATION: APPLICANT: Mitcham, Jen

Jennifer Lynn

US/09338933

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; SOFTWARE: FastSE; SEQ ID NO 5; LENGTH: 531; TYPE: DNA; ORGANISM: Homo sUS-09-404-879A-5
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Best Local Similarity 62.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.46222
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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                    GCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCC
                                                                              GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGGGATT
                                                                                                                                         GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCCTCCACACTTCCCCCT
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GGAAGCATGCCCAATCTGTCCATTCATCAGCCATTGCC
                                                            ATCATGAAACAACCCC-
                                                                                                                     ATATGGGCCTTATCAGATCTGAACAAGGATGGGAAGACCAGCAAGAGTTCTCTATA
                                                                                                                                                                                                 GGTGATCAAGCCCGTACTTTTTCCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAA
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                                                         -CTATGTTCTCTCCÁCTÁATCTCTGCTCGTTTTGGGÁTG
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US-09-215-681-5
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                                                                                                                    LENGTH: 531
TYPE: DNA
ORGANISM: Homo sapien
US-09-215-681-5
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TYPE: DNA
ORGANISM: Homo sapien
US-09-338-933-5
                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                      Best Local Similarity Matches 247; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09215681A Patent No. 6528253
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Best Local Similarity
                                                                             Query Match
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION UMBER: US/09/338,933
CURRENT APPLICATION UMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
CURRENT FILING DATE: 1999-06-23
                                                                                                                                                                                                                                                                                            APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REFERENCE: 210121.463
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Pred. No. 2e-26;
0; Mismatches 145; Indels
                                                           Score 144; DB 4; Length 531; Pred. No. 2e-26;
                                        Mismatches 145;
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RESULT 12
US-08-728-323A-1
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                                                                              TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
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           STRANDEDNESS:
TOPOLOGY: lin
                                              TYPE: nucleic acid
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STATE: New York
COUNTRY: U.S.A.
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CLASSIFICATION:
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Best Local Similarity 45.1%;
Matches 534; Conservative
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
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Patent No. 6322792
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Best Local Similarity
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APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: REPAINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REPERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
EARLIER FILING DATE: 1998-11-19
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TYPE: DNA
ORGANISM: Kaposi's
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SEQ ID NO 1
LENGTH: 3489
                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09410399 Patent No. 6482587
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                  APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
                                                      TYPE: DNA
ORGANISM: Kaposi's
-09-410-399-1
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                                     ĠĊĀĀĠĀGCAGGĀGGTGGAĀGAGCĀĀGĀGCAGGĀGCAGGAĀGAGCAGGAATTAGAGGAGGT 2597
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Best Local Similarity
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-08-770-379-20
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                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 522
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                          LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Russo, James J.
Edelman, Isidore S.
Moore, Patrick S.
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2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Allergic disease e	AA017881	23	1681	49.3	3091.5	9
Novel human diagno	ABG20575	22	932	49.4	3097.5	89
Human polypeptide	AAM43519	22	1035	68.2	4277	7
Novel central nerv	AAU87168	22	1031	68.2	4277	6
Human SH3D1A prot	AAY32154	20	1144	86.8	5442.5	ហ
Human SH3D1A prot	AAY32155	20	1220	93.3	5847.5	4
Human SH3D1A prot	AAY32156	20	1215	93.5	5860	ω
Mouse Esell protei	AAY57449	21	1715	99.8	6258.5	N
Mouse Esel protei	AAY57444	21	1214	99.8	6258.5	1
Description	ID	BB	Match Length DB	Match	Score	No.
				Query		Result
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45	44	43	42	41	40	39	38	37	36	35	3 4	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
486.5	503	503	527	535.5	535.5	536.5	536.5	536.5	536.5	536.5	536.5	572	572	572	572.5	712	774.5	816.5	1046	1183.5	1330.5	1361	1388.5	1536.5	1702	2058.5	2273.5	2812	3012	3034.5	3046	3049.5	3049.5	3068	3070.5
7.8	٠	8.0		8.5	•	•		8.6	8.6	8.6	•	•	9.1	9.1	9.1	11.4	12.4	13.0	16.7	•	21.2	21.7	22.1	24.5		•	36.3	٠	48.0	ω.	8	œ	48.6		49.0
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17	24	22	23	24	22	24	21	24	24	24	24	22	22	22	24	23	22	17	24	22	22	22	17	22	22	17	22	22	20	22	21	21	21	22	20
AAR92750	ABU03911	AAB95697	AAO20504	ABU03912	AAM40292	ABU03914	AAY86194	ABU03916	ABU03915 .	ABU03910	ABU03909	AAU19936	AAM43613	AAU87484	ABU71035	ABP41930	AA000069	AAW05396	ABU71097	AAB93738	AAU17173	AAU87256	AAW05399	ABG20576	ABB57814	AAW05395	AAM93676 ·	AAB94691	AAY32158	AAM93229	AAY71160	AAY57450	AAY57445	AAM79199	AAY32157
Human EGF receptor	Human expressed pr	Human protein sequ	Protein of APP rel	Human expressed pr	ο.	Human expressed pr	-				_		-				Human polypeptide	Human SH3P18 prote	_	protein				Novel human diagno			Human polypeptide,	Human protein sequ	Human SH3D1A prote	Human polypeptide,	Rat phosphodiester	Mouse Ese2L protei		protein	Human SH3D1A prote

ALIGNMENTS

AAY57444	SULT 1 Y57444
standard;	
Protein;	

1214 AA

Mouse Esel protein sequence.

28-FEB-2000 AAY57444;

(first entry)

Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking; regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral.

Mus sp.

WO9955728-A2.

04-NOV-1999.

27-APR-1998; 05-FEB-1999; 27-APR-1999; 98CA-2230201. 99US-0118739. 99WO-CA00375.

(HSCR-) HSC RES & DEV LP.

WPI; 2000-052802/04. N-PSDB; AAZ39008, AAZ39009. Egan SE, Wang W, Sengar A;

New nucleic acid encoding of endocytosis, used e.g. infection -

Page

43;

99pp;

English.

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The present sequence represents mouse Esel. The present invention CC specifically describes mammalian Esel and 2 proteins (I) and their splice CC variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) CC are involved in regulation of clathrin-mediated endocytosis (as a complex CC with Espl5 protein), vesicular trafficking and actin cytoskeleton. CC Generally (I) (or its (ant)agonists, mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); sequences antisense to the (I) CC polynucleotide, agents that downregulate expression of Ese genes or CC antagonists of an Ese binding partner are used to treat diseases CC associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Esel is used to block CC clathrin-mediated endocytosis in vivo or in cell cultures, while CC clathrin-mediated endocytosis in vivo or in cell cultures, while CC clathrin-mediated endocytosis in vivo or in cell cultures while CC clathrin-mediated to proliferate by a growth factor receptor; CC and similar compounds (also inactive Ese mutants) can be used to prevent CC viral infection. Endocytosis may also be regulated, in vivo or in cell C cultures, by forming an Ese-Espl5 complex, then binding dynamin to the CC complex. Generally conditions that can be treated include cancer; CC abnormal cell division or migration; viral infection; or abnormal CC complex. Generally conditions that can be treated include cancer;
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LIPEKQILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRSKLQEI
                                                                                            ELEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQQMLGR
                                                                                                                                                                                 QREEERRKEIERREAAKRELERQRQ-LEWERNRRQELLNQRNKEQEGTVVLKARRKTLEF
                                                                                                                                                                                                                                      SVELEKRROALLEQORKEGERLAQLERAEGERKERERGEGEAKRQLELEKGLEKGRELER
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treating cancer
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AC MOUS
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KW FESU
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tion; actin cytoskeleton; detection; cancer; infection;
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                                                                                                                                                                                                                                                                                                                                                             megakaryoctyic abnormality, myeloproliferative disorder, haematopoietic disorder, platelet disorder or leukaemia; and screening of drugs for cancer therapy.
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             PEYIPPSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQQP-EKKLPVTFEDKKRENFER
                                                              TGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPVLP
                                                                                             KSSSFSRSGPGSQLNTKLQKAQSFDVASVPPVAEWAVPQSSRLKYRQLFNSHDKTMSGHL
                                                                                                          KSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHL
                                                                                                                                            ASMPPLTAVAPVPMGSIPVVGMSPTLVSSVPTAAVPPLANGAPPVIQPLPAFAHPAATLP
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tive 39; Mismatches
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SH3D1A; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative dis
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                                                                                                                                                                                                                                                                  Query Match
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haematopoietic disorder; cognitive dysfunction; microcephaly;
lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy:
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                                 KSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHL
                                                                                             ASMPPLTAVAPVPMGSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWP
                                                                                                                                                         IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGGI
                                                                                                                                                                                                    MAQFPTPFGGSLDIWAITVEERAKHDQQFHSLKPISGFITGDQARNFFFQSGLPQPVLAQ
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                                                                                                                                                                                                                                                                  39;
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This sequence represents the protein encoded by the novel human Standard gene (see AAZ34570). SHADIA contributes to the development of platelets and the pathogenesis of leukaemias, both in general and in particular those involving the megakaryocytic lineage. The gene maps to the small candidate region for low platelets on thromosome 21. The protein includes SH3 domains and EH domains, both maintenance of the cytoskeleton. At least 3 isoforms of with maintenance of the cytoskeleton. At least 3 isoforms of SH3DIA exist (see AAY32154-58). The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, myeloproliferative disorder, platelet disorder, acute leukaemia, chromosome 21, low platelets in deletion for 21, association of cysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, microcephaly, lissencephaly, and colpocephaly. Methods are also provided: for suppressing cells unable to regulate themselves; screening for a somatic aleguacy of a treatment; monitoring tumour risk progress or megakaryocytic abnormality, myeloproliferative disorder, and copietic disorder, platelet disorder or leukaemia; and corresponderic disorder, platelet disorder or leukaemia; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3DlA; human; Down's syndrome; leukaemia; cancer; megakaryocytic abnormality; myeloproliferative disorder; platelet disorder; neural disorder; thromobocytopenia; haematopoietic disorder; cognitive dysfunction; microcephaly; lissencephaly; colpocephaly; holoprosencephaly; diagnosis; therapy.
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                   VKLISGPVRKSTSIDTGPTESPASLKRVASPAAKPAIPGEEFIAMYTYESSEQGDLTFQQ
                                                                         VLGQGEKVEGLQAQALYPWRAKKDNHLNFNKNDVITVLEQQDMWWFGEVQGQKGWFPKSY
                                                                                           VLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLEQQDMWWFGEVQGQKGWFPKSY
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18-APR-2000;
19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                      Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AlDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; respirator; wound healing; cell proliferation; skin aging;
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04-FEB-2000;
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                                                                                                                                           e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodefictency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabete and pituitary dwarfism, cancers and disorders at the cellular level e.g. testicular feminisation.
                                                                                                                                                                                                                                                                           novel central nervous system protein. (I) and polypeptides (II) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I) are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. nepplasms of the breast or liver, cardiovascular disorders e.g. nepplasms of the breast or liver, cardiovascular disorders
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17-NOV-2000;
            leukaemia, disorders involving neovascularisation e.g. mailgnancies, respiratory disorders e.g. monallergic rhintis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to
                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding a protein preventing, treating or ameliorating medical food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; SEQ ID No 686; 837pp; English
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                                                                EPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPATATGS
                                                                                                                PGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLPVTSS
                                                                                                                                                   KPAVQAPWSTAEKGPLTISAQENVKVVYYRALYPFESRSHDEITIQPGDIVMVDESQTGE
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tive 28; Mismatches
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RESULT 7 AAM43519

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                                                                                                                                                                                                                                                                                                                                             or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, ce .g. breest and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or crogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, ce conitis, (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological disease e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as myocardial ischaemias; ce pilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly cfrom WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Best Local 9
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human polynucleotides (AAI63803-AAI64012) and the encoded proteins (AAM434497-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The
                                                                                                                                                                                                                                                                                                                            Sequence
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                        TGSCLGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLP
                                                                         KSSSFSRSGPGSQLNTKLQKAQSFDVASVPPVAEWAVPQSSRLKYRQLFNSHDKTMSGHL
                                                                                          KSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHL
                                                                                                                          ASMPPLTAVAPVPMGSIPVVGMSPTLVSSVPTAAVPPLANGAPPVIQPLPAFAHPAATLP
                                                                                                                                       ASMPPLTAVAPVPMGSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWP
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                                       -GPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLP
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Liu C,
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2000US-0649167.
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CC and to produce other types of data and products dependent on DNA and conditions of amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed as pecification, but was obtained in electronic format directly from WIPO as ferming and products of the invention.
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Best Local Simi
Matches 603;
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                                                                                                                                                                   LALRETPAPLPVTSSEPSTTPNNWADPSSTWPSSSNEKPETDNWDTWAAQPSLTVPSAGQ
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                                  DMWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVASPAAKPAIPGEE
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MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQ

Query Match
Best Local Similarity
Matches 656; Conserv

Conservative 187;

49.3%;

Score 3091.5; DB 23; .Pred. No. 1.2e-189;

Length 1681;

Mismatches

274;

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                                                                                                                                         The present invention relates to a method for examining allergic diseases with intersectin 2 gene or a gene with equivalent function of intersectin 2 as an indicator gene, which comprises determining the expression level of the gene in the eosinophils in a patient, and comparing the expression level with that in the eosinophils of a healthy individual. The method is for examining allergic diseases, particularly atopic dermatitis, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugita Y,
Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOX
(NIGE-) JAPAN
(EISA) EISAI
      Sequence
                                                                                     for examining allergic diseases, particularly atopic dermatitis, we also applicable in screening candidate compounds for remedies. The present sequence is a human protein described in the exemplifications.
                                                                                                                                                                                                                                                                                                                                                                                                            Method for examining allergic diseases by differential display intersectin 2 gene showing different expression particularly significant increase in eosinophils in patients -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atopic dermatitis;
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                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 78-86; 90pp; Japanese.
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                                                             the invention.
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DB; AAL47247.
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                                                                 -REEPEALYAAVNKKPTSAAYSVGEEYIALYPYSSVEPGDLTFTEGEEILVTQKDGEWWT
                                                                                    PTESPASLKRVAS--PAAKPAIPGEEFIAMYTYESSEQGDLTFQQGDVIVVTKKDGDWWT
                                                                                                                                                   SWTAKKDNHLNFSKHDIITVLEQQENWWFGEVHGGRGWFPKSYVKIIPGSEVK-----
                                                                                                                                                                                                                                    OPASVTDYQN-VSFSNLTVNTSWQ--KKSAFTRTVSPG-SVSPIHGQGQVVENLKAQALC
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                          This sequence represents the protein encoded by the human SH3DIA CC cDNA clone 5 (see AAZ34573). SH3DIA contributes to the development CC of platelets and the pathogenesis of leukaemias, both in general cand in particular those involving the megakaryocytic lineage. The gene maps to the small candidate region for low platelets on CC chromosome 21. The protein includes SH3 domains and EH domains, CC both associated with protein-protein interactions and the latter CC with maintenance of the cytoskeleton. At least 3 isoforms of CC sH3DIA exist (see AAY32154-58). The invention provides methods for the diagnosis and treatment of megakaryocytic abnormality, cc myeloproliferative disorder, platelet disorder, acute leukaemia, CC neural disorders, thromobocytopenia, platelet disorder on CC chromosome 21, low platelets in deletion for 21, association of CC gains in chromosome 21 with leukaemias, neural abnormalities, CC dysfunctions and disorders including brain malformations and corresponding cognitive dysfunctions, malcrocephaly, liseencephaly, CC and colpocephaly. Methods are also provided: for suppressing CC cells unable to regulate themselves; screening for a somatic cells unable to regulate themselves; screening for a somatic caleguacy of a treatment; monitoring thmour risk progress or megakaryoctyic abnormality, myeloproliferative disorder, platelet disorder or leukaemia; and corrected of the corre
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                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemcopoissis regulating activity, tissue growth factor activity, hamunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                               Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides with useful in diagnosis and gene therapy -
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N-PSDB; AAK52332.
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Similarity 51.0%;
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Wang D,
Yang Y,
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n T, Goodrich R;
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Pred. No. 4.1e-188;
7; Mismatches 274;
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AAY57445
ID AAY57
XX AAY57
AC AAY57
XX AAY57
XX DT 28-FE
DT 28-FE
DX Mouse
XX Mouse
  Mouse; murine; Esel; Ese2; endocytosis; vesicular trafficking;
                                          Mouse Ese2 protein sequence
                                                                                   28-FEB-2000
                                                                                                                            AAY57445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEQERKERERQEGEAKRQLELEKQLEKQRELERQREEERRKEIERREAAKRELERQRQLE
                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                    KGEVSGQVGLFPSNYVKLTTDMDPSQQ 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSVEPGDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSNYVKPKDQESFGSASKSGASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESSEQGDLTFQQGDVIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVSPG-SVSPIHGQGQVVENLKAQALCSWTAKKDNHLNFSKHDIITVLEQQENWWFGEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLEQQDMWWFGEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTGEPGWLGGELKGKTGWFPANYAEKIP--ENEVPTPAKPVTDLTSAPAPKLALRETPAP
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                                                                                                                                                                                                                                                                        QGEINGVIGLEPSNYVKMTTDSDPSQQ 1192
                                                                                                                                                                                                                                                                                                                                                            KLLGPSSERATPAFHP-
                                                                                                                                                                                                                                                                                                                                                                               KLLSPGTSKITPTELPKTAVQPAVCQVIGMYDYTAQNDDELAFSKGQIINVLNKEDPDWW
                                                                                                                                                                                                                                                                                                                                                                                                                                         KKPEIAQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQGELQARGKKRQKGWFPASHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKPEIAQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGRGWFPKSYVKIIPGSEVK-----REEPEALYAAVNKKPTSAAYSVGEEYIALYPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVAS--PAAKPAIPGEEFIAMYTY 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPPTVSLSATS-----TSSEPLSSNQPASVTDYQN-VSFSNLTVNTSWQ--KKSAFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVGEPGWLYGSFQGNFGWFPCNYVEKMPSSENE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LATQAPWSTTEKGPLTISAQESVK-----VVYYRALYPFESRSHDEITIQPGDIVMVDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEERAKPEMQDKQSRLFHPHQEPAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LKELREIHSKQQLQKQRSLEAARLKQKEQERKSLELEKQK----EDAQRRVQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKKSLEKEELC-QRLKEQLDALEKETASKLSEMDSFNNQLKCGNMDDSVLQCLLSLLSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEVLDKQCDLEIMEIKQLQQELQEYQNKLIYLVPEKQLLNERIKNMQFSNTPDSGVSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIESTNKSRELRIAEITHLOOOLOESOOMLGRLIPEKQILSDOLKOVO-ONSLHRDSLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WERIRRQELLNQKNREQEEIVRLNSKKKNLHLELEALNGKHQQISGRLQDVRLKKQTQKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TLKAEEKKRETASVLVNYRALYPFEARNHDEMSFNSGDIIQVDEK
                                                                                   (first
                                                                                                                                                                     Protein;
                                                                                   entry)
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                                                                                                                                                                     1197
                                                                                                                                                                                                                                                                                                                                                         -VCQVIAMYDYAANNEDELSFSKGQLINVMNKDDPDWW
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CC with Esp15 protein), vesicular trafficking and actin cytoskeleton.

CC denerally (I) (or its (ant)agonists, minetics, fragments and inactive mutants); (I) specific antibodies (Ab); sequences antisense to the (I) polynucleotide; agents that downregulate expression of Ese genes or CC antagonists of an Ese binding partner are used to treat diseases CC associated with undesirable endocytosis and resulting changes in cellular function. Particularly overexpression of Ese 1 is used to block CC clathrin-mediated endocytosis in vivo or in cell cultures, while CC cantistion of (I) is used to promote endocytosis of selected cells. CC (Ant)agonists of (I) or Ab are used to suppress abnormal proliferation of CC cells that can be stimulated to proliferate by a growth factor receptor; CC and similar compounds (also inactive Ese mutants) can be used to prevent CC viral infection. Endocytosis may also be regulated, in vivo or in cell CC complex. Generally conditions that can be treated include cancer; CC complex. Generally conditions that can be treated include cancer; CC abnormal cell division or migration; viral infection; or abnormal compounds.
                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents mouse Ese2. The present invention specifically describes mammalian Ese1 and 2 proteins (I) and their splice variants (Ese = EH-domain and SH3-domain regulator of endocytosis). (I) are involved in regulation of clathrin-mediated endocytosis (as a complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation; actin cytoskeleton; detection; cancer; infection; EH-domain and SH3-domain regulator of endocytosis; anticancer; antiproliferative; antiviral.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding of endocytosis, used e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ39010, AAZ39011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-052802/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 33; Page 48; 99pp; English
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05-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-1999;
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    1197 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sengar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Esel and 2 proteins, involved in regulation for treating cancer or preventing viral
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밁 S 밁 Ś 밁 8 문 ঠ Query Match Best Local Similarity Matches 658; Conserv 165 174 120 61 61 VIQPLPAFAHPAATWPKSSSFS--RSGPGSQLNTKLQKAQS-FDVASAPP-----GIASMP-----PLTAVAPV--PMG-----SIPVVGMSPPLVSSVPPAAVPPLANGAPP 164 MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQ 60 LIQPL-SIPYSSSTLPHASSYSLMMGGFG---GASIQKAQSLIDLGSSSSTSSTASLSGN ---SMPNLSIHOPLPPVAPIATPLSSATSGTSIPPLMMPAPLVPSVSTSSLP---NGTAS 173 IWALSDLNKDGKWDQQEFSIAMKLIKLKLQGQQLPVVLPPIMKQPPMFSPLISA-RFGWG 119 | IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPV--AISSAPAFGIG 118 MAQFFTAMNGGPNMWAITSEERTKHDKQFDNLKPSGGYITGDQARTFFLQSGLPAPVLAE Conservative 177; 48.6%; Score 3049.5; DB 21 52.4%; Pred. No. 3.9e-187; ative 177; Mismatches 275; 21; Indels Length 1197; 145; Gaps 60 32

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212

----AAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSLPQAQLASIWNLS 26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPKTGTSEWAVPQPSRLKYRQKFNSLDKGMSGYLSGFQARNALLQSNLSQTQLATIWTLA
                                                                                                                                                                                                                                                                                                                                                                                                  YRALYPFESRSHDEITIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWERNERQELLNORNKEQEGTVVLKARRKTLEFELEALNDKKHQLEGKLQDIRCRLATQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRLPEEPSSEDEQQPEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERLAQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIDQDGKLTAEEFILAMHLIDVAMSGQPLPPVLPPEYIPPSFRRVRSGSGMSVISSSSVD
                            YTAQNDDELAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSNYVKLTTDMDPSQQ 1213
                                                                  KNTSGWWQGELQARGKKRQKGWFPASHVKLLGPSSERTMPT
                                                                                         KNPGGWWEGELQARGKKRQIGWFFANYVKLLSPGTSKITPTELPKTAVQPAVCQVIGMYD
                                                                                                                                                                                                PASLKRVASPAAKPAIP-GEEFIAMYTYESSEQGDLTFQQGDVIVVTKKDGDWWTGTVGD
                                                                                                                                                                                                                         NHLNFSKHDVITVLEQQENWWFGEVHGGRGWFPKSYVKLIPGNEVQRGEPEALYAAVTKK
                                                                                                                                                                                                                                          NHLNFNKSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISG-PVRKS--TSIDTGPTES
                                                                                                                                                                                                                                                                             --TW------QQKSAFTRTVSPG-SVSPIHGQGQAVENLKAQALCSWTAKKE
                                                                                                                                                                                                                                                                                                                                                         PTPAKPVTDLTSAPAPKLALRETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDN
                                                                                                                                                                                                                                                                                                                                                                                                                                        EKSQDKTQEEER---KAEAKQSE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEVLDKQCDLEIMEIKQLQQELKEYQNKLIYLVPEKQLLNERIKNMQLSNTPDSGISL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EWERLRROELLSOKTREOEDIVRLSSRKKSLHLELEAVNGKHQQISGRLQDVQIRKQTQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIDGDGQLKAEEFILAMHLTDMAKAGQPLPLTLPPELVPPSFR-----GGKQV---DSVN
                                                                                                                   RTGIFPSNYVRPKDQENFGNASKSGASNKKPETAQVTSAYAASGTEQLSLAPGQLILILK
                                                                                                                                                                                                                                                                                                                                                                                   YRALYPFEARNHDEMSFSSGDIIQVDEKTVGEPGWLYGSFQGKFGWFPCNYVEKVLSSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARLKOKEGERKSLE-LEKOK---EDAGRRVGERDKOWLEHVQGEEGPRPRKPHEEDRLKR
                                                                                                                                                                                                                                                                                                                                 -KALSPKKALLPPTVSLSATSTS-SOPPASVTDYHNV--SFSNLTVNT--
                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TASA-----LVN
                                                                 ---FHAVCOVIAMYD
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RESULT 13 AAY57450

RXU

AAY57450; AAY57450

standard; Protein; 1658

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119 120

GIASMP-----PLTAVAPV--PMG-----SIPVVGMSPPLVSSVPPAAVPPLANGAPP 164

---SMPNLSTHQPLPPVAPTATPLSSATSGTSTPPLMMPAPLVPSVSTSSLP---

NGTAS

IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPV--AISSAPAFGIG MAQFPTAMNGGPNMWAITSEERTKHDKQFDNLKFSGGYITGDQARTFFLQSGLPAPVLAE

118 119

60 60

IWALSDLNKDGKMDQQEFSIAMKLIKLKLQGQQLPVVLPPIMKQPPMFSPLISA-RFGMG

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CC The present invention specifically describes mammalian Esel and 2 CC proteins (I) and their splice variants (Ese = EH-domain and SH3-domain CC regulator of endocytosis). (I) are involved in regulation of clathrin-CC mediated endocytosis (as a complex with Espl5 protein), vesicular CC trafficking and actin cytoskeleton. Generally (I) (or its (ant)agonists CC mimetics, fragments and inactive mutants); (I)-specific antibodies (Ab); CC sequences antisense to the (I) polynucleotide; agents that downregulate CC used to treat diseases associated with undesirable endocytosis and CC resulting changes in cellular function. Particularly overexpression of Esel is used to block clathrin-mediated endocytosis in vivo or in cell CC cultures, while administration of (I) is used to promote endocytosis of CC selected cells. (Ant)agonists of (I) or Ab are used to suppress abnormal CC proliferation of cells that can be stimulated to proliferate by a growth CC cused to prevent viral infection. Endocytosis may also be regulated, in CC vivo or in cell cultures, by forming an Ese-Espl5 complex, then binding CC cancer; abnormal cell division or migration; viral infection, or abnormal CC receptor signalling, tissue development or synaptic transmission. The CC present sequence represents mouse Ese2I protein sequence.
                                                                                  Query Match
Best Local Sim
Matches 658;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding Esel and 2 proteins, involved in regulation of endocytosis, used e.g. for treating cancer or preventing viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1999;
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1 MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKFIAGFITGDQARNFFFQSGLPQPVLAQ
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99US-0118739.
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                                                                                  177;
                                                                                      Score 3049.5; DB 2
Pred. No. 6.1e-187;
'7; Mismatches 275;
                                                                                                                                                    DB 21;
                                                                                      Indels 145;
                                                                                                                                             Length 1658;
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EWERNRRQELLNQRNKEQEGTVVLKARRKTLEFELEALNDKKHQLEGKLQDIRCRLATQR
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                                                                                                 KNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTELPKTAVQPAVCQVIGMYD 1158
                                                                                                                                                        RTGIFPSNYVRPKDQENFGNASKSGASNKKPEIAQVTSAYAASGTEQLSLAPGQLILILK
                                                                                                                                                                                            KSGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYAATGPEQLTLAPGQLILIRK 1098
                                                                                                                                                                                                                                                       PASLKRVASPAAKPAIP-GEEFIAMYTYESSEQGDLTFQQGDVIVVTKKDGDWWTGTVGD
                                                                                                                                                                                                                                                                                                                NHLNFSKHDVITVLEQQENWWFGEVHGGRGWFPKSYVKLIPGNEVQRGEPEALYAAVTKK
                                                                                                                                                                                                                                                                                                                                        NHLNFNKSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISG-PVRKS--TSIDTGPTES
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                                                                                                                                                                                                                                     PTS---TAYPVTSTAYPVGEDYIALYSYSSVEPGDLTFTEGEEILVTQKDGEWWTGSIGE
                                                                                                                                                                                                                                                                                                                                                                                         -----QQKSAFTRTVSPG-SVSPIHGQGQAVENLKAQALCSWTAKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KALSPKKALLPPTVSLSATSTS-SQPPASVTDYHNV--SFSNLTVNT--
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밁 ð 밁 ঠ 占 ર્ 밁 5 밁 ঠ 밁 S 밁 8 밁 Ş 밁

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MAQFFTFFGGSLDVWAITVEERAKHDQQFLSLKFIAGFTTGDQARNFFFQSGLFQFVLAQ MAQFPTAMNGGPNMWAITSEERTKHDKQFDNLKPSGGYITGDQARTFFLQSGLPAPVLAE

187;

Indels

Gaps

61

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ARESULT 14
AAY71160
ID AAY71
XX AAY71
XX OB-SH
XX Rat;
XX Rat;
XX Rat;
XX Rat;
XX Rat;
XX Conju
XX antii
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XX A
                                                                                                                                                                                                                                     The present sequence is a phosphodiesterase (PDE) interacting protein, CC M14 from rat. The protein modulates the functions and properties of PDEs, CC specifically cAMP-PDEs, and also targets them to specific subcellular CC compartments. The present sequence CC can be used in the diagnosis and treatment of disease conditions CC associated with PDE activity. The disease include asthma, cystic CC fibrosis, inflammatory airway disease, chronic bronchitis, cosinophilic CC granuloma, psoriasis, proliferative skin disease, endotoxic shock, CC septic shock, ulcerative colitis, Crohn's disease, reperfusion injury, CC inflammatory airway disease, urticaria, adult respiratory CC distress syndrome, diabetes insipidus, allergic rhinitis, allergic conjunctivitis, vernal conjunctivitis, arterial restenosis, atheroselerosis, inflammatory diseases associated with irritation and CC atheroselerosis, inflammatory diseases associated with irritation and CC pain, rheumatoid arthritis, antylosing spondylitis, transplant creftion and graft versus host disease, disease conditions associated with hypersecretion of gastric acid, and disease conditions in which
       Query Match
Best Local S
Matches 652
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                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide encoding a phosphodiesterase (PDE) interacting polypeptide, useful for diagnosis and treatment of asthma, cyfibrosis, Crohn's disease, and rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; phosphodiesterase interacting protein; M14; PDE; CAMP-PDE; cyclic adenosine monophosphate phosphodiesterase; antiacthmatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide, useful for dia
fibrosis, Crohn's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71160 standard; Protein; 1683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1999;
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652; Conserv
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48.6%;
nilarity 50.8%;
Conservative 187
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       Score 3046; DB 21;
Pred. No. 1.1e-186;
7; Mismatches 267;
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                                                                                                                                                                                             ATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLEQQDMWWFGEVQGQ
                                                                                                                                                                                                                                                                                  VTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPAT
                                                                                                                                                                                                                                                                                                                                                        GWLGGELKGKTGWFPANYAEK-IPENEVPTPAK----PVTDLTSAPAPKLALRETPAPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENLWKESIRKEEE-----EKQKRLQEEKSQDRTQEEER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNLFLLLKELRESYNTOOLALEOLHKI KRDKLKELERKRLEOIOKKKLEDEAARKAKOGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTLPSYQKTQ-EEEPQKKLPVTFEDKRKANYERGNMELEKRRQVLMEQQQREAERKAQKE
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EQGDLTEQQGDVIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKKP 1069
                                                                                                         KGWFPKSYVKLISGPVRKSTSIDTGPTES-PASLKRVASPAAKPAIPGEEFIAMYTYESS
                                                                                                                                                              SPG-SVSPIHGOGQAVENLKAQALCSWTAKKENHLNFSKHDVITVLEQQENWWFGEVHGG
                                                                                                                                                                                                                                            LCSNQPAPV----TDYQNV--SFSNLNVNT----TW------QQKSAFTRTV 869
                                                                                                                                                                                                                                                                                                                          GWLYGSFQGKFGWFPCNYVEKMLSSDKTPSPKKALLPPAVSLSATSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                              LATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVMVDESQTGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEERAKPEMQDKQSRLFHPHQEPAK
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                                                                                                                                                                                                                                                                                                                                                                                                          -KTEAKQSETARA------LVNYRALYPFEARNHDEMSFNSGDIIQVDEKTVGEP
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Best Local Sim
Matches 603;
                                                                       The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                              830 Primers useful for synthesizing use in genetic manipulation -
                                                     Sequence
                                                                                                                                                                                                                                                      Claim 8;
                                                                                                                                                                                                                                                                                                                        N-PSDB; AAK94139.
                                                                                                                                                                                                                                                                                                                                                                           Ota T,
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02-MAY-2000;
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                                                                                                                                                                                                                                                    SEQ ID NO 2647; 1380pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPSAERTTP----AFHAVCQVIAMYDYIANNEDELNFSKGQLINVMNKDDPDWWQGE
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                                                     642 AA;
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2000JP-0183765
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na T, Nagai
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Score 3034.5; DB 2
Pred. No. 1.5e-186;
B; Mismatches 20;
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K, Kojima
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541 LIPEKQILNDQLKQVQQNSLHRDSLVTLKRALEAKELARQHLRDQLDEVEKETRSKLQEI 600
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DVFNNQLKELREIHSKQQLQKQRSLEAARLKQKEQERKSLEL 641
|:||||||||||:||||||:|| ||||||||| :||
DIFNNQLKELREIHNKQQLQKQKSMEAERLKQKEQERKIIEL 642
                                                                                                                                                                      PEYIPPSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQQP-EKKLPVTFEDKKRENFER 359
                                                                                                                                                                                                                                                                                                                                             TGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPVLP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IWALADMINIDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGGI 120
                                                                                                               ELEALNDKKHQLEGKLQDIRCRLTTQRQEIESTNKSRELRIAEITHLQQQLQESQQMLGR
                                                                                                                                ELEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQQMLGR
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Search completed: December 4, 2003, 15:18:34 Job time : 45 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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506.3
406.4
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383.5
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centrosome associa	T08621	N	2442	4.7	293	Ü
myosin II heavy ch	T47237	N	746	4.7	294	4
hypothetical prote	T50989 .	2	729	4.7	295	43
plectin - rat	A39638	1	4687	4.7	. 296	Ň
ALR protein - h	T03454	2	5262	4.7	296.5	Ξ
ALR protein - huma	T03455	2	4957	4.7	296.5	Ö
hypothetical prote	T34418	2	3488	4.7	296.5	9
nuclear mitotic ap	A42184	้	2101	4.7	297	α
serine/threonine p	T30989	2	1233	4.8	299	7
plectin (imported)	A59404	2	4684	4.8	302	0
kinetoplast-associ	A44937	<u>,</u>	1052	4.8	302	ū
hypothetical prote	S47179	2	956	4.9	304.5	4
involucrin - humar	A24168	ь.	585	4.9	304.5	w
h-caldesmon - chio	A33430	_	771	4.9	306.5	N
NF-180 - sea lampı	151116	2	1110	4.9	307.5	<u>, , , , , , , , , , , , , , , , , , , </u>
probable erythrocy	T09127	2	1701	4.9	308.5	0

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RESULT

adaptor protein intersectin - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: T09194
R;Yamabhai, M.; Hoffman, N.G.; Hardison, N.L.; McPherson, P.S.; Castagnoli, L.; Ces J. Biol. Chem. 273, 31401-31407, 1998
A;Title: Intersectin, a novel adaptor protein with two eps15 homology and five src A;Reference number: Z16605; MUID:99030416; PMID:9813051
A;Accession: T09194
A;Status: preliminary; translated from GB/EMBL/DDBJ δ 뮍 Ś 밁 Ş 문 δ 밁 Ś 밁 δ 밁 A;Molecule type: mRNA A;Residues: 1-1270 <YBM> A;Cross-references: EMBL:AF032118; NID:g2642624; PIDN:AAC73068.1; PID:g2642625 A;Experimental source: cell type oocyte ş C; Keywords: endocytosis A; Description: involved in endocytosis Query Match 80.8%; Best Local Similarity 80.6%; Matches 358 359 238 239 178 179 121 119 980; 61 13 1 MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQ RGSVELEKRRQALLEQQRKEQERLAQLERAEQERKERERQEQEAKRQLELEKQLEKQREL 418 HLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPV WPKSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSG GIASMPPLTAVAPVPMGSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAAT 178 TWALADMINIDGRMDQLEFSIAMKLIKLKLQGYPLPSILPSNMLKQPVAMPAAAVAGFGMS IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLDSTLPPVMKQQPVAISSA--PAFGIG MAQFGTPFGGNLDIWAITVEERAKHDQQFHGLKPTAGYITGDQARNFFLQSGLPQPVLAQ LPPEYIPPSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQQPEKKLPVTFEDKKRENFE LPKSSSFGRSVAGSQINTKLQKAQSFDVPAPPLVVEWAVPSSSRLKYRQLFNSQDKTMSG GIVGIPPLAAVAPVPMPSIPVVGMSPPLVSSVP--TVPPLSNGAPAVIQSHPAFAH-SAT LPPEYIPPSFRRVRSGSGLSIMSSVSVDQRLPEEPEEEEPQNADKKLPVTFEDKKRENFE Hoffman, N.G.; Hardison, N.L.; McPherson, P.S.; Castagnoli, L.; Cesareni 273, 31401-31407, 1998 Conservative ; 86 Score 5063.5; Pred. No. 2.7e-98; Mismatches 7e-198; DB 2; 123; Indels Length 1270; 15; Gaps 358 118 357 297 298 120 237 177 60 238 homol

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RESULT 2
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dynamin associated protein isoform 160-2 - fruit fly (Drosophila medynamin associated protein isoform 160-2 - fruit fly (Drosophila medynamin associate C;Species: Drosophila medanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-C;Accession: T13055
R;Roos, J.; Kelly, R.B.
J. Biol. Chem. 273, 19108-19119, 1998
A;Title: Dapi60, a neural-specific Eps15 homology and multiple SH3
A;Reference number: Z17594; MUID:98334647; PMID:9668096
A;Accession: T13055
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rosidues: 1-1011 <ROO>
A;Cross-references: EMBL:AF054612; NID:g2996029; PID:g2996030; PID:
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                     QQDMWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVASPAAKPAIPG
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                                                                                    GQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLE
                                                                                                                    PVAAV-EAPVDAQVADT
                                                                                                                                                    PKLALRETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSA
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                                                      --ADLTAAG
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RESULT 4 731-504 731-504 731-504 hypothetical protein Y116A8C.36 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: 731504 R;KcMutray, A. submitted to the EMBL Data Library, October 1999 A;Reference number: Z21041 A;Accession: T31504 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1097 <wil> A;Cross-references: EMBL:AL117204; PIDN:CAB55138.1; CESP:Y116A8C.36 A;Experimental source: clone Y116A8C</wil>	Qy 1058TAGKT	Qy 818 PKLALRETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSA 877	Qy 474 RKTLEFELEALNDKKHQLEGKLQDIRCRLATORQEIESTNKSRELRIAEITHLQQQLQES 533 Db 454 NTQLNVELSTLNEKIKELSQRICDTRAGVTNVKTVIDGMRTQRDTSMSEMSQLKARIKEQ 513 Qy 534 QQMLGRLIPEKQILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLR 582

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                      KSDVITVLEQQDMWWFG-EVQGQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVA 987
                                                      AMGLTEGGA-
                                                                                   QPSLTVPSAGQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFN
                                                                                                                                                                                     FEARSEDELSFEPGDVIIVFQSHAAEPGWRAGQLREKVGWFPEAFVEAIA--AVPTPG--
                                                                                                                                                                                                                  FESRSHDEITIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKP
                                                                                                                                                                                                                                                    TDASQRFDADFGATST-----ADPFAQIAQAP--AHSKGAVDQSAFNIHDTYKCRALFA
                                                                                                                                                                                                                                                                                   KEAEERAKPEMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYP
                                                                                                                                                                                                                                                                                                                                                   KEDAQRRVQERDKQWLEHVQQEEQPRPRKP------HEEDRLKREDSVRK
                                                                                                                                                                                                                                                                                                                                                                                   LELSTEKEKSYNQTEILKTNKEKYKTDVYSK-----LVAKREEYRNSFEL---
                                                                                                                                                                                                                                                                                                                                                                                                                  -EVERETRSKLQEIDVF-NNQLKELREIHSKQQLQKQRSLEAARLKQKEQERKSLELEKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQQREKTLQFQLQALDEKVIDVEVDIGKAKEAVAEVTGFIERMRSTRDEKVARI----KE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REEEEKKRRLEMERRREEDEKMRKVQMEKAKVKQMQVQMPEQKKWNFYNQKQQENERLAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELV------RMCGISSRSANNTPELEPGAEPPQ--KSPAPKTFEDKRQDNLSKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYIPPSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQQPEKKLPVTFEDKKRENFERGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPOARTILMOSSLPOAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPVLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSRHNSISAGSPLN-----NDRNVFEGRQLENWAIPHHNKLKYSQLFNALDKERLGSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKDGRLDIREYSIAMRLALNCLAGIPIPPQLPPSLLVVPA--RNAPPTWPGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGGIASMPPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEVSDAEYQKNFAMF-----GQLTGGQPFMDAVTARNALMRSNLPTQVLSQIWALSDL
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                                                                                                                   -----AARKAEI----AA
                                                                                                                                                   VTDLTSAPAPKLALRETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAA
                                                                                                                                                                                                                                                                                                                   ----LVHAQTHARSKIGEFEAKSAPASAAPAPAPAPATTTNGFPANFNDAFGEFD----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQETNQ---KTAIESQELGHQL--LQKQSAHKET-TQRKSELEALRRKRDAIRKAIEDAA
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                                                      -PPASSAPAAAAVIS------QCIAQFQWRARNEEDLSFA
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submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid ZK1248.
A;Reference number: Z21534
A;Accession: T34490
A;Stattus: preliminary; translated from GB/EMBL/DDBJ
A;Stattus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-751 <LAT>
A;Residues: 1-751 <LAT>
A;Cross-references: EMBL:UZ9244; PIDN:AAC71084.1; GSPDB:GN00020; CESP:ZK1248.3
A,Experimental source: strain Bristol N2; clone ZK1248
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ZK1248.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change C;Accession: T34490 #sequence_revision 29-Oct-1999 #text_change R;Latreille, P.
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A;Map position: 2
A;Introns: 37/1; 74/3; 118/3; 355/2; 661/1; 728/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPITPTDQAKYDSIFQSLNPVNGKLSGAHVRPVLMNSGLDAHALARIWELSDQDKDGNLD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIEMSVÄLHLVYRSLQSDPVPAQLPPNLIHPSKAMYAHSSPNF-----AAPP---HPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVEFSIAMKLIKLKLQGYQLPSTLPP--VMKQQPVAISSAPAFGIGGIASMPPLTAVAPV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- RATAVYDYEASOPDELGFKTGDVIIVTDKSEAEWWSGHREODPSKSGLFPSNYVQ 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCQVIGMYDYTAQNDDELAFSKGQIINVLNKEDPDWWKG---EVSGQVGLFPSNYVK 1203
                                          NFERGSVELEKRROALLEOORKEQERLAQLERAEQERKERERQEQEAKROLELEKQLEKQ 415
                                                                                                                                                                                   KDGLVDGMDMRAPMMTTGLSAQILAHVWALADIKKCGQLNLEQFALTMHLLDMAKRGESI 368
                                                                                                                                                                                                                             MSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPL 295
                                                                                                                                                                                                                                                                             GASTPISASHS-----YADQFAQTDTN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGEIVKIREKSAAGWWEGELIRNGKP-IAGWFPGEYVKVLEEAASPAT------
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NEE--MKQLAESIQSMLVERKTAEEAVLQLE-ADMTIKNSSIK----NLQVELATLESTV
                                                                                                                                                                                                                                                                                                                                                                    PMMGSRAGSVTSLDDVNMSQS-YSATMPRAYPP-----
                                                                                                                                    PPVLPPEYIPPSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQQPEKKLPVTFEDKKRE 355
                                                                                                                                                                                                                                                                                                                     -ATWPKSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKT 235
                                                                                                                                                                                                                                                                                                                                                                                                            PM-----GSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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RESULT 6
A54696
EGF recep
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A;Residues: 1-897 <FAZ>
A;Cross-references: GB:L21768; NID:g404756;
C;Superfamily: calmodulin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF receptor substrate eps15 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
C;Accession: A54696
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F;48-69/Domain: calmodulin repeat homology <EF1>
F;160-192/Domain: calmodulin repeat homology <EF2>
F;23-255/Domain: calmodulin repeat homology <EF3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: eps15, a novel tyrosine kinase substrate, exhibits A;Reference number: A54696; MUID:93361014; PMID:7689153 A;Accession: A54696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Fazioli, F.; Minichiello, L.; Matoskova, Mol. Cell. Biol. 13, 5814-5828, 1993
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                                 NTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSL 254
                                                                                                     GSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWPKSSSFSRSGPGSQL 194
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Pred. No. 1e-12;
     WVVSPAEKAKYDEIFLKTDKDMDGYVSGLEVRETFLKTGL
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A;Cross-references: EMBL:Z29064; NID:g470034; PIDN:CAA82305.1; PID:g4 R;Wong, W.T.; Kraus, M.H.; Carlomagno, F.; Zelano, A.; Druck, T.; Crc Oncogene 9, 1591-1597, 1994
A;Tille: The human eps15 gene, encoding a tyrosine kinase substrate, A;Reference number: I38525; MUID:94239734; PMID:8183552
                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-896 <BER>
                                                                                                                                 R;Bernard, O.A.; Mauchauffe, M.; Mecucci, Concogene 9, 1039-1045, 1994
A;Title: A novel gene, AF-1p, fused to HRX
A;Reference number: S43074; MUID:94181254;
A;Accession: S43074
                                                                                                                                                                                                                     epidermal growth factor receptor substrate - human c;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Date: 11-Jan-1995 #sequence revision 13-Jan-1995 #text_change 01-Dec-2000 C;Accession: S43074; I38525
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-821,'M',823-896 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Gene: GDB:EPS15; AF-1P; MLLT5
;Cross-references: GDB:360337; OMIM:600051
;Map position: 1p32-1p32
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                                   781 ---ELKGKTGWFPAN-----YAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494 KLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILSDQLKQ 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 NTNLQKLQAQKQ-----QVQELLDE------------LDEQKAQLEE 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 WAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQIWALADMNNDGRMD 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLKEVRKKCAEEAQLISSLK-----AELTSQESQISTYEEELAK-----AREELSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQREK-----NNVEQDLKEKE------DTIKQRTSEVQ---DLQDEVQRE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAM-SGQPLPPVLPPEYIPPSFRRVRS 313
NEDPFRSATSSSVSNVVITKNVFEETSVKSEDEPPALP-----PKIGTPTRPCPLP
                                                                                                            KVVYYRALYPFESRSHDEITIQPGDIVMVDESQT-----GEPGWLGG------
                                                                                                                                                 DPFVGSDPFKDDPFGKIDPFGGDPFKGSDPFASDCFFRQSTDPFATSSTDPFSAANNSSI
                                                                                                                                                                                     ----AKPEMQDKQSRLFHPHQEPAK-----LATQAPWSTTEKGPLTISAQESV
                                                                                                                                                                                                                            VTDENEVTTAVTEKVCSELDN------NRHSKEEDPFNVDSSSLTGPVADTNLDFFQS
                                                                                                                                                                                                                                                                 EKQKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEER------
                                                                                                                                                                                                                                                                                                       WCSSPHSILVNGATDYCSLSTSSSETANLNEHVEGQSNLESEPIHQESPARSSPELLPSG
                                                                                                                                                                                                                                                                                                                                          ELREIHS------KQQLQKQRSLEAARLKQKEQERKSLEL----
                                                                                                                                                                                                                                                                                                                                                                                LQQETAE-----LEESVESGKAQLEPLQQHLQDSQQEISSMQMKLMEMKDLENHNSQLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KT------WVVSPAEKAKYDEIFLKTDKDMDGFVSGLEVREIFLKTGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGGIASMPPLTAVAPVPM 134
                                                                      -----ETLKHNDPFAPGGTVVAASDSATDPFASVFGNESFGGGFADFSTLSKVN
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Q q - L - Q - Q	ed to the EMBL Data Library ence number: \$58703 sion: \$58706 ule type: DNA ues: 1-1480 <vos> -references: EMBL:X79743 H.; Tamames, J.; Teodoru, 1, 61-78, 1995 : Nucleotide sequence and a ence number: \$50795 MUID:9 sion: \$50795 sion: \$7080001445; osition: \$7080001445; osition: \$7080001445; osition: \$7080001445; osition: \$7080001445;</vos>	OY 831VTSEP

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PIPPSVTQEPPVPLAPPLPAVDGFQEPPIPSAPAIATAVQKSGSSTPALAGGVLPPP---
                                                                                                                                                                                                                                                                                                                                 STWPSSSNE-----KPETDNWDTWAAQPSLTVPSAGQLRQRS-AFTPATATGSSPSPVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                     AEKI PENEVPTP----AKPVTDLTSAPAPKLALRETPAP--LPVTSSEPSTTPNNWADFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QESVKVVYYRALYPFESRSHD-EITIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFGGHVNVPQAAPVAPSAAFSQNSTNAPRSVHAAVTPAAGKNSTGLPSTTMGHNPYFKDA 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAKQESDDEDEDDEEKRLQEELKRLKKKKADKEKRLAALRKQIEDAQNESDEEETNGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAORRVOERDKOWLEHVOOEEOPRPRKPHEEDRLKR-----EDSVRKKEAEE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVLKARRKTLEFE-LEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEKQLEKQRELERQREEERRKEIERREAAKRELERQRQLEWERNRRQELLNQRNKEQEGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROALLEOORKEOER----
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                                     GAQPVSTAGIPSIP 1469
                                                                                             GWFPKSYVKLISGP 965
                                                                                                                                                                                                              QGEKVEGLQAQALYPWRAKKDNHLNFNK-----SDVITVLEQQDMWWFGEVQGQK 951
                                                                                                                                                                                                                                                                                                                                                                                         DNKVEEAKIGHPDHARAPPV---TAAPLPSV----TPVPPAVPVPQANTSNEKSSPIPIA 1345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QEFERWEFGIGLEDGVREFL-DDLKSNSNKSVTESSPFVPSSTPTPVDDRSSSPSYSQF
                                                                                                                                                         --PPLPTQQASTSEPIIAHVDNYNGAEKGTGAYGSDSDDDVLSIPES--
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                                                                                                                                                     -VGTDEEEE 1455
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A;Experimental source: strain S288C
R;Scherens, B.; el Bakkoury, M.; Vierendeels, F.; Dubois, E.; Messenguy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: strain S288C
R;Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy,
submitted to the Protein Sequence Database, August 1994
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A;Title: The sequence of a 22.4 kb DNA fragment from the left arm of years.
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A;Cross-references: EMBL:Z23261; NID:g313733; PIDN:CAA80797.1;
A;Experimental source: strain S288C
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A;Title: Sequencing and functional analysis of a 32 560 bp segment on the left A;Reference number: S39824; MUID:94205266; PMID:8154187
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A; Residues: 1-961 <GOF>
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A; Residues: 579-1381
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A; Residues: 579-1381 < DUB>
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A; Accession: S45782
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A; Residues: 1-961 < DEF>
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A;Experimental source: strain S288C
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Matches 286
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TMSGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQP
                                                                                                                   PAATWPKSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDK
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                                                                                                                                                                                                                                       FGIGGIASMPPLTAVAPVPMGSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAH
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20.0%; Pred. No. 4e-09;
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                                                           -ASDWSLSFEKKQQFDAIFDSLDK
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966VRISTSIDTGPTESPASLKRVASFAAKPALP-GEFIAMYTYESSEGGILTFQGG	870 PSLTVPSAGQLRQ 063 ASTDVLS 924HLNFNKS : : : 115 EFPPIQELHIDES	714AKLATQAPWSTTEKGPLTISAGESVKVVYYRALYPFESRSHDEI	49 DOLKOVOON :	383AQLERAEQERKERERQEGEAKROLELEKQLEKORELERQREGERRKEIER 587 QDLFADGEASAQLSNATTEMANLSNQVNSLSKQASITNDKKSRATQELKRVTEMKNSIQI 433 REAAKRELERQRQLEWERNRRQELLNQRNKEQEGTVVLKARRKTLEFELEALNDKKHQLE 587 QDLFADGEASAQLSNATTEMANLSNQVNKEQEGTVVLKARRKTLEFELEALNDKKHQLE 647 KLNNLRSTHDQNVKQTEQLEAQVLQVNKENETHAQQLAVSEANYHAAE 493 GKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQMLGRLIPEKQILS 595 SKLNELTTDLQESQTKNAELKEQITNLNSMTASLQSQLINEKQQ	291 QHAGSLSSAVLVPFFFLSSRLNQETLATIWDLADIHNNAEFTKLEFAIAMFLIQKKNAGVE 295 LPPVLPPEYIPPSFRRVRSGSGMSVISSSS
GEEFLAMYTYESSEGGDLTFQGD 1020	ALYPWRAKKDN- 923 :	AQESVKVVYYRALYPFESRSHDEI 757		LEKQLEKQRELERQREEERRKEIER 432 : : :	

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RESULT 11
A45592
Liver stage antigen LSA-1 - malaria parasite (Plasmodium falciparum)
Liver stage antigen falciparum
C;Species: Plasmodium falciparum
C;Date: 22-Nov-1993 #sequence revision 02-Dec-1994 #text change 09-Jun-2000
C;Accession: S24597; A45592; S29393; S34842; B45592; C45592; D45592
R;Zhu, J.; Hollingdale, M.

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Дb	Ş	Db	Q	Дb	Ş	유 &	Db	Qy	рb	Ş	당 왕	Ö	. 8	Query M Best Lo Matches	A; Introns: A; Introns: C; Superfami C; Keywords: F; 49-81/Dom	A; Molecule A; Residues A; Cross-re C; Comment: Covalent m	submitt A;Descr A;Refer A;Acces	S28589 trichohyalir C;Species: C;Date: 12-N C;Accession: R:Fietz. M.ii	RESULT	В	Qy	ρb
612 LLQEREERLRRQERERKLREEEQ 635	680 LKREDSVRKKEAEERAKPEMQ 700	553 LOREKRO-EREREYREEEKLOREEDEKRROEREROYRELEELROEEQLRORKLREEEQ 611	624 LEAARLKQKEQERKSLELEKQKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDR 679	93 RAQQLQEEDSFQEDRERRRRQQEQRPGQTWRWQLQEEAQRRRHTLYAKPGQQEQLREEEEE 5		532 -ESQQMLGRLIPEKQILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQ 580	377 ORQLESEAGARQSKYYSRPRRQEEQSLRODQERRQRQERERELEEQARRQQQWQAE 432	TLEFELEALNDKKHQLEGKLQDIRCRLATQRQ	: RREQRLEQEERREQQLXRELEEIR	427 RKEIERRE-AAKRELERQRQLEWERNRRQELLNQRNKEQEGTVVLKAR 473	376REOERLAQLERAEQERKEREKQEGEAKRQLELEKQLEKORELEKOREEER 426	EETIBEEQLXXXBQQBLXXBLXBBEQQXXBXXBQHBXALQBBEEQLLXQXXXXBBBTXBQQ 23	DQRLPEEPSSEDEQQPEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQ	Match 6.2%; Score 391.5; DB 1; Length 1407; Local Similarity 29.7%; Pred. No. 1.2e-08; Les 132; Conservative 97; Mismatches 140; Indels 75; Gaps 18;	C;Genetie: A,Intronm: 46/3 C;Superfamily: trichohyalin; calmodulin repeat homology C;Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat F;49-81/Domain: calmodulin repeat homology <ef2></ef2>	A;Molecule type: DNA A;Residues: 1-1407 <fis> A;Cross-references: EMBL:Z19092; NID:g1746; PIDN:CAA79519.1; PID:g1747 A;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root she C;Volment modifications to this protein include conversion of arginine to citrulline and t</fis>	d to the EMBL I ption: Examinat nce number: S28 ion: S28589	rabbit bryctolagus cun lar-1993 #seque S28589	10	1296 GNSKAEPTKVATPSIPQQPIPLKNDPIVDASLSKGPIVN 1334	PKTAVOPAVCQVIGMYDYTAQNDDELAFSKGQI	1273 QQ QSTSDPAQVSNDEWD-EIFAGF 1295

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A;Molecule type: DNA
A;Residues: 323-381,'HKAI' <GUE2>
A;Cross-references: EMBL:M28266
A;Note: difference at carrboxyl end due to frameshift error C;Comment: This protein is found as flocculent material in C;Superfamily: trichohyalin; calmodulin repeat homology C;Keywords: EF hand
C;Keywords: EF hand
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A; Molecule type: DNA
A; Residues: 1-195;638-688;1165-1215;1590-1909 </
A; Residues: 1-195;638-688;1165-1215;1590-1909 </
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A;Description: a liver-stage-sepcific antigen of plasmodium falciparum char A;Reference number: S34842
A;Accession: S34842
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Nature 329, 164-167, 1987
A;Title: A liver-stage-specific antigen of Plasmodium falciparum characterized by A;Reference number: S29393; MUID:87315391; PMID:3306406
A;Accession: S29393
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A;Residues: 1-1909 <ZHU>
A;Cross-references: EMBL:X56203; NID:g9915; PID:g9916
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A;Molecule type: DNA
A;Residues: 323-387 <GUE1>
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MOl. Biochem. Parasitchi. 48, 223-226, 1991
A;Title: Structure of Plasmodium falciparum liver stage
A;Reference number: A45592; MUID:92107224; PMID:1840628
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                                                                                         RLAKEKLOEQOSDLEQERRAKEKLOEQOSDLEQDRLAKEKLOEQORDLEQERRAKEKLOE
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28.3%; Pred. No. 3.6e-08;
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A;Molecule type: DNA
A;Residues: 1-1898 <LEE>
A;Residues: 1-1898 <LEE>
A;Residues: 1-1898 <LEE>
A;Cross-references: GB:L09190; NID:g292835; PIDN:AAA65582.1; PID:g292836
A;Note: authors translated the codon AGG for residue 1714 as Pro
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root
C;Covalent modifications to this protein include conversion of arginine to citrulline ar
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C;Date: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
C;Accession: A45973
R;Lee, S.C.; Kim, I.G.; Marekov, L.N.; O'Keefe, E.J.; Parry, D.A.D.; Steinert, J. Biol. Chem. 268, 12164-12176, 1993
A;Title: The structure of human trichohyalin. Potential multiple roles as a fur ed (cross-linking) protein.
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A45973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A45973; MUID:93280194; PMID:7685034 A;Accession: A45973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trichohyalin - human
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PQEQEEKRRRESELQWQEEERAHRQQQEEEQRRDFTWQWQAE-----EKSERGRQRLS
                                                PHEEDRLKREDSVRKKEAEERAKPEMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTIS
                                                                                                LKREHEEERREQELAEEEQEQARERIKSRIPKWQWQLESEADARQSKVLLEAPQAGRAEA
                                                                                                                                                                                              QEERRDERLKREEPEBERRHELLKSEEQEERRHEQLRREQQERREQRLKREEBEBRLEQR
                                                                                                                                                                                                                                                                                              REEEKRLEQERREQRLKREQEERRDQLLKREEERRQQRLKREQEERLEQRLKREEVERLE
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                                                                                                                                           ----EQERKSLEL-EKQKEDAQRRVQERDKQWLEHVQQEEQPRPRK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%; Score 381; DB 1; ilarity 27.0%; Pred. No. 4.5e-08; Conservative 117; Mismatches 159
                                                                                                                                                                                                                                                                                                                                    -GRLIPEKQILSDQL----KQVQQNSLHRDSLLTLKRALEAKELARQQ
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RESULT
T15597
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C;Superfamily: trichohyalin; calmodulin repeat homology
C;Keywords: calcium binding; citrulline; EF hand; hair;
F;49-81/Domain: calmodulin repeat homology <EF2>
F;387-851/Region: 28-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
(;Date: 21-Sep-1993 #sequence revision 01-Mar-1996 #text_change 22-Jun-1999
C;Accession: A40691; A34209; S32633
R;Fietz, M.J.; McLaughlan, C.J.; Campbell, M.T.; Rogers, G.E.
J. Cell Biol. 121, 855-865, 1993
A;Title: Analysis of the sheep trichohyalin gene: potential structural and A;Reference number: A40691; MUID:93260018; PMID:7684041
A;Accession: A40691; MUID:93260018; PMID:7684041
A;Accession: A40691; MUID:93260018; PMID:7684041
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A;Cross-references: EMBL:Z18361; NID:g295940; PIDN:CAA79165.1; A;Note: sequence extracted from NCBI backbone (NCBIP:132511)
R;Fietz, M.J.; Presland, R.B.; Rogers, G.E.
J. Cell Biol. 110, 427-436, 1990
A;Title: The cDNA-deduced amino acid sequence for trichohyalin, A;Reference number: A34209; MUID:90130632; PMID:2298812
A;Accession: A34209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1016-1151,1205-1257,1281-1398,'G',1400-1549 <FI2>
A;Cross-references: GB:X51695; NID:g1827; PIDN:CAA35992.1; PID:g1828
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root she covalent modifications to this protein include conversion of arginine to citrulline and
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Best Local Similarity
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                                                                          RRQERERQYLEKEELQRQEE---RLQREKEQLQREDREKRRQVRERKYLEEELQQEEDRL
                                                                                                                  RVQERDKQWL--EHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEER--AKPEMQDKQSRL 706
                                                                                                                                                         QERERQYLEKELQRQEERLQEEEQLLREEREKRRQERERQYLEKVELQEEEQLQREEREK
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  QPMYYTTREPEVTTKVERQVIERIDRNVWVEDVPYAPSQS
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R;Favello, T.
submitted to the EMBL Data Library, October 1995
** Pagarintion: The sequence of C. elegans cosmid
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A;Experimental source: strain Bristol N2
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A; Accession: T15597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 MSG--HLTGPQARTILMQS--SLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 KSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNS-----HDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSKQQLQKQRSL-EAARLKQKEQERKSL---BLEKQKEDAQRRVQERDKQWLEHVQQEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QRQLEWERNRRQ----ELLNQRNKEQEGTV---VLKARRKTLEFELEALNDKKHQLEGKL
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APLPVTSSEPSTTP-
                                                                                                             VDESQTGEPGWLGGELKGKTGWFPANYAEKI PENEVPTPAKPVTDLTSAPAPKLALRETP
                                                                                                                                                                     RERANEEAQLADLLERERHNQLIRENERREAVERANNRRLE--DRRSRDKL-----DHIV
                                                                                                                                                                                                                             FHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVM
                                                                                                                                                                                                                                                                                   KRRQEEEEEIARLNELQRAAAARQAQRNAELDRQRQRDELDRK-AQELSEREMREKERRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPEKKLPVTFEDKKRENFERGSVELEKRRQ-----ALLEQQRKEQERLAQLERAEQER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSDEYYRREVMTRTIITRSTEALSQTPL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88/3; 126/3; 433/2; 494/2; 711/2
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1.1e-07;
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P 826	VDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETP	Qy 767
v 603 .	REFANESAQLADLLERERHNQLIRENERREAVERANNRRLEDRRSRDKLDHIV	Db 551
4 766	FHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVM	Qy 707
550	KRRQEEEEEIARLNELQRAAAARQAQRNAELDRQRQRDELDRK-AQELSEREMREKERRD	Db 492
706	REDSVRKKEAEERAKPEMQDK	Оу 669
R 491	ERKEEERREFELIEAARRKKEARDRORLDEMERERVREEEERREKERREQERRIAAEKER	Db 432
2 668	QOLQKQRSL-EAARLKQKEQERKSLELEKQKEDAQRRVQERDKQWLEHVQQ	Оу 613
R 431	RRREEERREAELVADVHRQAEERERLRKRQEREEAERLERIRLEQQKIDMERIDAERRER	Db 372
I 612	-QONSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRSKLQEIDVFNNQL-KELREI	Qy 555
4 371	RILRERIELERIERERRELEARERQELELQRREAEDRERQRLEDEAREM	Db 323
V 554	QDIRCRLATQROEIESTNKS-RELRIAEITHLQQQLQESQQMLGRLIPEKQILSDQLKQV	Qу 496
- 322	ER-LEEERROKEKAETERIERERREHERIEIERIKRERIERERREREEKKAEED	Db 267
495	RQLEWERNRRQELLNQRNKEQEGTVVLKARRKTLEFELEALN	Оу 443
266	REKKRREEWDRLESIRLAEEEABLARRRALEKER-IDREKAEEERKTWERLERERARLER	Db 208
R 442	RQEQEAKRQLELEKQLEKQREL	Оу 393
20	QQNLSERALAERERADKERLQQ-ERLL	Db 149
392	QPEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERLAQLERAEQER	Qy 340
2 148	GRPASPLDRYLPYPTTTTTTSGDGRT-REEKTVDYKVTYHRDIEEQERRIREDQARRQ	Db 92
2 339	GQPLPPVLPPEYIP-PSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQ	Оу 292
91	PSDEYYRREVMTRTIITRSTEALSQTPL	Db 64
8 291 .	- 23	Оу 236
63	TSTYE	Db 7
r 235	KSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKT	Qy 181
32;	5.7%; Score 359.5; DB 2; Length 1017; Similarity 23.6%; Pred. No. 1.6e-07; P; Conservative 142; Mismatches 270; Indels 169; Gaps	Query Match Best Local Matches 17
73/2	CESP:C25A11.4a CESP:C25A11.4a .s: 65/3; 88/3; 126/3; 433/2; 494/2; 711/2; 735/1; 792/3; 833/3; 87	;Gene: ;Intron
1.1; CESP:C25A1	es: 1-1017 <fav> references: EMBL:U39650; NID:g1049376; PID:g1049380; PIDN:AAA80391 mental source: strain Bristol N2</fav>	A;Residues: 1-1 A;Cross-referen A;Experimental
	preliminary; translated from GB/EMBL/DDBJ type: DNA	** ** **
	the EMBL Data Library, October 1995 1: The sequence of C. elegans cosmid C25All. 1: The sequence of C. elegans cosmid C25All.	400
999	Caenorhabditis elegans Caenorhabditis elegans Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-199 T. T15598	C;Species: Ca C;Date: 20-Se C;Date: 20-Se C;Accession:
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P34216 saccharomyc
P37709 oryctolagus
P37709 oryctolagus
Q07283 homo sapien
P22793 ovis aries
Q05281 homo sapien
O95819 homo sapien
O95819 homo sapien
Q10172 schizosacch
Q9259 rattus norv
Q8r550 mus musculu
Q96b97 homo sapien
P46504 caenorhabdi
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Q15811 homo sapien
Q42287 xenopus lae
Q9nzm3 homo sapien
Q92076 mus musculu
P42566 mus musculu
Q91zu8
Q91Jq0
P12957
P07476
P07476
Q40554
Q15149
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P90425
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Q95V73
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5 cricetulus
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M21_STRPY	DYNA_NEUCR	CING HUMAN	DC11_DROME	NCK1_HUMAN	CING XENLA	GARP PLAFF	LVA DROME	GLT DROME	MYS AEQIR	INVO_HYLLA	INVO AOTTR
P50468 streptococc	Q01397 neurospora	Q9p2m7 homo sapien	P18169 drosophila	P16333 homo sapien	Q9ptd7 xenopus lae	P13816 plasmodium	Q8mss1 drosophila	P33438 drosophila	P24733 aequipecten	P17941 hylobates l	

ALIGNMENTS

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ity). ANEOUS: Overexpression results in the inhibitic rrin uptake and the blockage of the clathrin-me osis. ITY: Contains 1 C2 domain. ITY: Contains 1 DBL-homology (DH) domain.	ISOId=Q9ZOR4-2; Sequence=VSP_004296; -i-TISSUE SPECIFICITY: Widely expressed. Expressed at high levels in brain, heart and skeletal musclei- DOMAIN: SH3-3, SH3-4 and SH3-5, but not SH3-1 and SH3-2 domains, bind to dynamin (By similarity)i- DOMAIN: The KLERQ domain binds to SNAP-25 and SNAP-23 (By		"Mouse homologues of human chromosome 21 genes."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. -I- FUNCTION: Adapter protein that may provide indirect link between the endocytic membrane traffic and the actin assembly machinery. May regulate the formation of clathrin-coated vesicles. -I- SUBUNIT: Interacts with dynamin, SNAP-25 and SNAP-23. Clusters several dynamin in a manner that is regulated by alternative splicing. Also binds clathrin-associated proteins and other components of the endocytic machinery, such as N-WASp, Eps15 and Stonin 2 (By similarity).	SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE-99164083; pubMed=10064583; Sengar A.S., Wang W., Bishay J., Cohen S., Egan S.E.; Sengar A.S., Wang W., Bishay J., Cohen S., Egan S.E.; "The EH and SH3 domain Ese proteins regulate endocytosis by linking to dynamin and Eps15."; EMBO J. 18:1159-1171(1999). [2] [2] [2] [3] [2] [3] [4] [5] [6] [7] [8] [8] [9] [9] [9] [10] [1	HT 1 MOUSE STANDARD; PRT; 1714 AA. OPZOR4; Q9R143; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 11-SEP-2003 (Rel. 47, Last sequence update) 11-SEP-2003 (Rel. 47, Last sequence update) 11-SEP-2003 (Rel. 47, Last sequence update) 11-SEP-2003 (Rel. 47, Last sequence update) 11-SEP-2003 (Rel. 47, Last sequence update) 11-SEP-2003 (Rel. 47, Last sequence update) 11-SEP-2003 (Rel. 41, Created) 11-SEP-2003 (Rel. 41, Creat

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Pfam; PF00621; RhoGEF; 1.

Pfam; PF00621; RhoGEF; 1.

Pfam; PF00621; SH3JOMAIN.

ProDom; PD000066; SH3; 5.

PRINTS; PR00023; C2; 1.

SMART; SM00024; EFh; 2.

SMART; SM00024; EFh; 2.

SMART; SM00025; RhoGEF; 1.

SMART; SM00325; RhoGEF; 1.

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SMART; SM00325; RhoGEF; 1.

PROSITE; PS00004; C2_DOMAIN_2; 1.

PROSITE; PS50001; DH 2; 1.

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PROSITE; PS50010; DH 2; 
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EMBL; AF132478; AAD19746.1; -.
EMBL; AF169621; AAD48848.1; -.
EMBL; AF36517; AAV40228.1; -.
HSSP; P29354; 1GFC.
MGD; MGI:1338069; ITSN.
InterPro; IPR000008; C2.
InterPro; IPR002048; EF-hand.
InterPro; IPR002048; EF-hand.
InterPro; IPR000189; PH.
InterPro; IPR000189; PH.
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1 PH domain.
5 SH3 domains.
2 EH domains.
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EF-HAND 1 (POTENTIAL).

EH 2.

EF-HAND 2 (POTENTIAL).

LYS/LEU/GLU/ARG/GLN-RICH (ICOILED COIL (POTENTIAL).

SH3 1.

SH3 2.

SH3 3.

SH3 4.

SH3 5.

DH.

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C2 DOMAIN.

POLY-SER.

Missing (in isoform 2).

/FIGHOUSP 004296.

/FIGHOUSP 004296.
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Pred. No. 3.9
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                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restrease by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                        Pfam; PF00036; efhand; 3. Pfam; PF00018; SH3; 5. ProDom; PD000066; SH3; 5.
                                                                                                                                           EMBL; AF127798; AAD30271.1;
EMBL; AF132672; AAD31026.1;
HSSP; P29354; IGFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99303609; PubMed=10373452;
Okamoto M., Schoch S., Suedhof T.C.;
"EHSH1/intersectin, a protein that contains EH and
binds to dynamin and SNAP-25. A protein connection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Intersectin 1 (EH domain and SH3 domain regulator of endocytosis 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9WVĒ9;
                                                                                InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EPS15_homology.
InterPro; IPR001452; SH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITSN1 OR ITSN OR EHSH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 274:18446-18454(1999).

FUNCTION: Adapter protein that may provide indirect link between the endocytic membrane traffic and the actin assembly machinery.

May regulate the formation of clathrin-coated vesicles.

SUBUNIT: Interacts with dynamin, SNAP-25 and SNAP-23. Clusters several dynamin in a manner that is regulated by alternative splicing. Also binds clathrin-associated proteins and other components of the endocytic machinery, such as N-WASp, Eps15 and Stonin 2 (By similarity).

SUBCELULUAR LOCATION: Cytoplasmic; membrane-associated protein.

Enriched in synaptosomes.
                                                                                                                                                                                                                                                                                                                                                                              bind to dynamin.

DOMAIN: The KLERQ domain binds to SI
SIMILARITY: Contains 2 EP-hand calc:
SIMILARITY: Contains 5 SH3 domains.
SIMILARITY: Contains 2 EH domains.
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DOMAIN: SH3-3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocytosis?";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9WVE9-2; Sequence=VSP_004297; SSUE SPECIFICITY: Highly expressed in MAIN: SH3-3, SH3-4 and SH3-5, but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q9WVE9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comment=Additional isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9WVE1;
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SM00326; SH; 5.

; PS00018; EF HAND;

; PS50031; EH; 2.

; PS50002; SH3; 5.
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EHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEERAKPEMQDKQSRLFHPHQEPAKLATQA
                                                                                        VFNNQLKELREIHSKQQLQKQRSLEAARLKQKEQERKSLELEKQKEDAQRRVQERDKQWL
                                                                                                                                                                                                                                          LEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQQMLGRL
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                                                                                                                                                                            I PEKQI LSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRSKLQEID
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EF + HAND 1 (POTENTIAL).

EH 2

EF + PAND 2 (POTENTIAL).

LYS/LEU/GLU/ARG/GLN-RICH (COILED COIL (POTENTIAL).

SH3 1.

SH3 2.

SH3 3.

SH3 4.

SH3 5.

SH3 9.

POLY-SER.

Missing (in isoform 2).

/FTId=VSP_004297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
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); Mismatches
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Intersectin 1 (SH3 domain-containing protein 1A)
                                                                                          Pucharcos C., Fuentes J.-J., Casas C., de la Luna S., Alcanta: Arbones M.L., Soriano E., Estivill X., Pritchard M.; "Alu-splice cloning of human intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome."; Eur. J. Hum. Genet. 7:704-712(1999).
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=99415290; PubMed=10482960;
                                                                                                                                                                                                                                                                                                                                                                                   "Two isoforms of a human intersectin (ITSN) protein are produced brain-specific alternative splicing in a stop codon."; Genomics 53:369-376(1998).
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Antonarakis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Fetal brain;
TISSUE-Fetal brain;
MEDLINE-99017974; PubMed-9799604;
MCDLINE-99017974; PubMed-9799604;
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Mammalia; Eutheria; Primates;
                                 SEQUENCE OF
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Cytogenet. Cell Genet. 78:213-215:1197/).

-i- FUNCTION: Adapter protein that may provide indirect link between the endocytic membrane traffic and the actin assembly machinery. May regulate the formation of clathrin-coated vesicles. Isoform is could be involved in brain-specific synaptic vesicle recycling.
-i- SUBUNIT: Interacts with dynamin, SNAP-23 and SNAP-23. Clusters several dynamin in a manner that is regulated by alternative splicing. Also binds clathrin-associated proteins and other splicing. Also binds clathrin-associated proteins and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pucharcos C., Casas C., Nadal M., Estiv
"The human intersectin genes and their
differentially expressed.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tayba L.O., Kvasha S.M., Skripkina I.Y., Anopy
Tassone F., Rynditch A.V., Gardiner K.;
"Mouse homologs of human chromosome 21 genes."
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sparks A.B., Hoffman N.G., McConnell S. "Cloning of ligand targets: systematic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98294438;
                                                            SIMILARITY: Contains 1 DBL-homology (DH) domain SIMILARITY: Contains 2 EF-hand calcium-binding SIMILARITY: Contains 1 PH domain. SIMILARITY: Contains 5 SH3 domains. SIMILARITY: Contains 5 SH3 domains.
                                                                                                                                                                                                                           ISOIG-Q15811-4; Sequence=VSP_004294;
ITSSUE SPECIFICITY: Ubiquitous in adult and fetal tissues, excisoform 1 which is expressed almost exclusively in the brain. Highly expressed in skeletal muscle, heart, spleen, ovary, tes and all fetal tissues tested. Expressed at lower levels in the blood, lung, liver and pancreas. Isoform 1 is expressed in all brain regions; not expressed in the spinal cord.

DOMAIN: SH3-3, SH3-4 and SH3-5 but not SH3-1 and SH3-2 domains bind to dynamin (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compositions (By similarity).

Stonin 2 (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic; membrane-associated convicted in synaptosomes (By similarity).
                                                                                                                                                                                              gimilarity)
DISEASE: Ove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event-Alternative splicing; Named isoforms-4,
Comment-Additional isoforms seem to exist. Alternative splicing
affects domains involved in protein recognition and thus may
play a role in selecting specific interactions;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1; Synonyms=Long, ITSN-1;
IsoId=Q15811-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enriched in synaptosomes ALTERNATIVE PRODUCTS:
                                                                                                                                                SIMILARITY: Contains 1 C2 domain.
                                                                                                                                                             suggesting a gene dosage-dependent abnormalities of Down syndrome
                                                                                                                                                                                                                                                                                                                                                                                                Name=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H., Antonarakis S.E.;
SH3D1A gene maps to human chromosome 21q22.1-->q22.2.";
genet. Cell Genet. 78:213-215(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q15811-2; Sequence=VSP_004295;
ame=3; Synonyms=Short 2, SH3P17;
                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q15811-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biophys. Acta 1521:1-11(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synonyms=Short, ITSN-s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marrow;
                                                                                                                                                                                                Overexpressed in brain
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                                                                                                                                                                              dosage-dependent
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence=VSP_004293, VSP_004294,
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their spliced variants
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copyright. It is produced through a c tute of Bioinformatics and the EMBL ics Institute. There are no restrict

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Genew; HGNC:6183; ITSN1.

MIM; 602442; -.

GO; GO:0005509; F:calcium ion binding; GO; GO:005509; F:guany;-nucleotide ext InterPro; IPR00008; C2.

InterPro; IPR0002048; EF-hand.
InterPro; IPR000201; EF015 homology.
InterPro; IPR000219; RhoGEF.
InterPro; IPR0001849; PH.
InterPro; IPR000185; C2; 1.

Pfam; PF00168; C2; 1.

Pfam; PF00038; efhand; 3.

Pfam; PF00038; HANGEF; 1.

Pfam; PF00018; SH3; 5.

PRINTS; PR00499; P67PHOX.

PRINTS; PR00499; P67PHOX.

PRINTS; PR00452; SH3DOMAIN.

PRODOM; PD000066; SH3; 5.

PRINTS; PR00452; SH3DOMAIN.

PRODOM; PD000066; SH3; 5.

SMART; SM00023; C2; 1.

SMART; SM00023; C2; 1.

SMART; SM00023; C2; 1.

SMART; SM00023; EFh; 2.

SMART; SM00023; RH; 1.

SMART; SM00023; PH; 1.

SMART; SM00023; PH; 1.

SMART; SM00023; SH3; 5.

PROSITE; PS50004; C2 DOMAIN.

PROSITE; PS50001; DH 2; 1.

PROSITE; PS50002; SH3; 5.

Endocytosis; SH3 domain; Repeat; Coiled Alternative splicing; 3D-structure.

DOMAIN 326 702 LYS/LEU/GJ
DOMAIN 326 702 LYS/LEU/GJ
DOMAIN 1002 1060 SH3 1.

DOMAIN 1002 1060 SH3 3.

DOMAIN 1002 1583 SH3 SH3 4.

DOMAIN 1155 1214 SH3 5.

DOMAIN 1237 1423
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EMBL; AF064247; AAC80437.1; JOINED.
EMBL; AF064245; AAC80437.1; JOINED.
EMBL; AF064246; AAC80437.1; JOINED.
EMBL; AF064243; AAC78610.1; -.
EMBL; AF114488; AAD29953.1; -.
EMBL; AF114487; AAD29953.1; -.
EMBL; AF114487; AAD29952.1; -.
EMBL; AF114487; AAD29952.1; -.
EMBL; AF114487; AAD29952.1; -.
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EH 1.

EF-HAND 1 (POTENTIAL).

EH 2.

EF-HAND 2 (POTENTIAL).

LYS/LEU/GLU/ARG/GLN-RICH (COLLED COIL (POTENTIAL).

SH3 1.

SH3 2.

SH3 3.

SH3 4.

SH3 4.

SH3 5.

DH.

C2 DOMAIN.

Missing (in isoform 3).
  /FTId=VSP 004293.
Missing (In isoform 3
/FTId=VSP 004294.
Missing (In isoform 2
/FTId=VSP 004295.
P -> A (IN REF. 2)
T -> A (IN REF. 3).
G -> N (IN REF. 1).
S -> N (IN REF. 2).
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PIR; T09194; T09194.
HSSP; P29355; ISEM.
InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EF915_homology.
InterPro; IPR000108; Neu-Cyt_fact_2.
InterPro; IPR001452; SH3.
Pfam; PF00036; efhand; 2.
Pfam; PF00036; SH3; 5.
PRINTS; PR00499; P67PHOX.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 5.
SMART; SM00054; EPh; 2.
SMART; SM00027; EH; 2.
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                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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PROSITE; PS00018; EF HAND;
PROSITE; PS50031; EH; 2.
PROSITE; PS50002; SH3; 5.
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                                                                                                                     NLTGPQARTILMQSSLPQSQLATIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPI
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  QIPWMNTEKAPLTIN-QGDVKVVYYRALYPFDARSHDEITIEPGDIIMVDESQTGEPGWL
                                                                              ERQREEERRKEIERREAAKRELEROROLEWERNRROELLNORNREGEDIVVLKAKKKTLE
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EH 1.
EF-HAND 1 (POTENTIAL).
EH 2.
EF-HAND 2 (POTENTIAL).
LYS/LEU/GLU/ARG/GLN-RICH (NOTED COIL (POTENTIAL).
SH3 1.
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SH3 3.
SH3 4.
SH3 5.
SH3 5.
SH3 5.
SH3 5.
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Pred. No. 2.56
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).

TISSUE=Fetal brain, and Fetal liver;

MEDLINE=20382722; PubMed=10922467;

Pucharcos C., Estivill X., de la Luna S.;

"Intersectin 2, a new multimodular protein mediated endocytosis.";

FERG TAFF AND TO THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE 
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnotation updat
Intersectin 2 (SH3 domain-containing protei
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Seifert M., Engel M., Welter C.;
"Intersectin 2 (SH3D1B), human homolog of mouse Ese2 pro
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
  SEQUENCE
                                                                                                                               Ohara O.
                                                                                                                                               MEDLINE=20039619; PubMed=10574462;
Nagase T., Ishikawa K.-I., Kikuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                          TISSUE=Brain;
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ITSN2 OR SH3D1B OR SWAP OR KIAA1256.
                                                                                                       Prediction of
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                                        ediction of the coding se complete sequences of 10 large proteins in vitro. Res. 6:337-345(1999).
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N.A.
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100 new cDNA clones from t
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protein:1B)
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i; Hominidae;
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                                                                                  brain
                                                                                                       human genes.
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  1261-1696
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IsoId=Q9NZM3-2; Sequence=VSP_003892;
Name=3; Synonyms=TTSN2-S1;
IsoId=Q9NZM3-3; Sequence=VSP_003893, VSP_003894;
Name=4; Synonyms=TTSN2-S2; SH3P18;
IsoId=Q9NZM3-4; Sequence=VSP_003895;
IsoId=Q9NZM3-4; Sequence=VSP_003895;
IsoId=Q9NZM3-4; Sequence=VSP_003895;
IsoSUB SPECIFICITY: Ubiquitous. Isoform 1 is primarily expression adult heart and liver.
In adult heart and liver.
IMISCELLANEOUS: Overexpression results in the inhibition of the transferrin uptake and the blockage of the clathrin-mediated
           EMBL;
EMBL;
                                                        EMBL;
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                               -!- FUNCTION: Adapter protein that may provide indirect link between the endocytic membrane traffic and the actin assembly machinery.

May regulate the formation of clathrin-coated vesicles.
-!- SUBUNIT: Belongs to a complex that may contain multimers of ITSN ITSN and Bps15, and different partners according to the step in
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MEDILNE=2154828; PubMed=11690630;
Pucharcos C., Casas C., Nadal M., Estiv
"The human intersectin genes and their
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Sparks A.B., Hoffman N.G., McConn
"Cloning of ligand targets: system
containing proteins.";
Nat. Biotechnol. 14:741-744 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 821-1284 FROM N.A. (ISOFORM 1). Wilson L.A., Fields D., Cruz L., Friesen J., & "SH3P18-like wasp associated protein (SWAP): F containing protein that interacts with WASP.", Submitted (APR-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project."; "NEDO human cDNA sequencing project."; "Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                        entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                      use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differentially expressed.";
Biochim. Biophys. Acta 1521:1-11(2001).
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Nishikawa T., Nagai
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TISSUE=Embryo;
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SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
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           AF182199;
AF248540;
AB033082;
                                                          AF182198; AAF59903.1;
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BAA86570.1;
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S., Takahash
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Pfam; PF00036; efhand; 2.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
Pfam; PF00018; SH3; 5.
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EMBL; AK000305; BAA91068.1; -.
EMBL; AF001630; AAD00899.1; -.
EMBL; U61167; AAC50593.1; -.
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InterPro; IPR000261; EPS15 hc
InterPro; IPR001849; PH.
InterPro; IPR000219; RhoGEF.
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Genew; HGNC:6184;
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                                              MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFGQSGLPQPVLAQ
  IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPV--AISSAPAFGIG 118
                              MAQFPTAMNGGPNMWAITSEERTKHDRQFDNLKPSGGYITGDQARNFFLQSGLPAPVLAE
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R -> G (IN REF. 4).

R -> G (IN REF. 5).

KANGSPK -> FAAAST (IN REF. 5).

WFPKSYV -> EFAAAST (IN REF. 6).

GEKMPVQ -> VDAAANS (IN REF. 5).

GEKMPVQ -> VDAAANS (IN REF. 5).

K -> Q (IN REF. 2 AND 3).

Y -> Y (IN REF. 2 AND 3).
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KKPEIAQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYV
                                           SSVEPGDLTFTEGEEILVTQXDGEWWTGSIGDRSGIFPSNYVKPKDQESFGSASKSGASN
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                                     InterPro;
InterPro;
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EMBL; AF132480; AAD19748.1;
HSSP; P29355; 1SEM.
MGD; MGI:1338049; Sh3d1B.
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                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITSN2 OR SH3D1B OR E
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Intersectin 2 (SH3 domain-containing protein 1B) (EH and SH3 domains protein 2) (EH domain and SH3 domain regulator of endocytosis 2).
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28-FEB-2003 (Re
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Name=2; Synonyms=Ese2, Short;
IsoId=Q9ZOR6-2; Sequence=VSD_003896, VSP_003897;
TISSUE SPECIFICITY: Widely expressed in adult tissues.
DEVELOPMENTAL STAGE: Widely distributed throughout the adult forebrain. Prominent expression was observed in the neocortex, the piriform cortex, the pyramidal cell layers of hippocampus, the piriform cortex, the pyramidal cell layers of hippocampus, the
                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                       and in the amygdala.

SIMILARITY: Contains 2 C2 domains.

SIMILARITY: Contains 1 DBL-homology (DH) domair

SIMILARITY: Contains 1 EPH domain.

SIMILARITY: Contains 1 PH domain.

SIMILARITY: Contains 5 SH3 domains.

SIMILARITY: Contains 2 EH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic (By similarity). ALTERNATIVE PRODUCTS:
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IsoId=Q9Z0R6-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                           non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGEINGVTGLFPSNYVKMTTDSDPSQQ 1191
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IPR000008; C2.
IPR002048; EF-hand.
IPR000261; EPS15_homology.
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Eutheria; Rodentia;
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thi; Muridae; Murinae; Mus.
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SMART; SM00024, EFh; 2.
SMART; SM00027; EH; 2.
SMART; SM00027; EH; 2.
SMART; SM00233; PH; 1.
SMART; SM00233; RhoGEF; 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00325; SH3; 5.
PROSITE; PS50004; C2 DMAIN_2; 1.
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50010; EF; HAND; 1.
PROSITE; PS50013; EH; 2.
PROSITE; PS50003; PH DMAIN; 1.
PROSITE; PS50003; PH DMAIN; 1.
PROSITE; PS50002; SH3; 5.
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                                                                                                VIQPLPAFAHPAATWPKSSSFS--RSGPGSQLNTKLQKAQS-FDVASAPP---
                                                                                                                       ---SMPNLSIHQPLPPVAPIATPLSSATSGTSIPPLMMPAPLVPSVSTSSLP--
                                                                                                                                         GIASMP-----PLTAVAPV--PMG-----SIPVVGMSPPLVSSVPPAAVPPLANGAPP
                                                                                                                                                              IWALSDLNKDGKWDQQEFSIAMKLIKLKLQGQQLPVVLPPIMKQPPMFSPLISA-RFGMG
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                                    SPKTGTSEWAVPQPSRLKYRQKFNSLDKGMSGYLSGFQARNALLQSNLSQTQLATIWTLA
                                                                               LIQPL-SIPYSSSTLPHASSYSLMMGGFG---GASIQKAQSLIDLGSSSSTSSTASLSGN
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IPR001452; SH3.
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IPR001849; PH.
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EF-HAND (POTENTIAL).
EH 2.
COILED COIL (POTENTIA SH3 1.
SH3 2.
SH3 3.
SH3 4.
SH3 5.
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/FILE="USP 003897.
KQ -> NT (IN REF. 1; AAD19748).
KQ -> (TN REF. 1; AAD19748).
                                                                                                                                                                                                                                               Score 3049.5; DB 1
Pred. No. 1.9e-109;
7; Mismatches 275;
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RESULT 7

EP15 — EP15

AC P425

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OS HOM
                    protein)
EPS15 OR
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01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Epidermal growth factor receptor substrate 15
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                                                                                                                                                                                                                                                                YMANNEDELNESKGOLINVMNKDDPDWWQGETNGLTGLFPSNYVKMTTDSDPSQQ
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    (Human)
                                                                                                                                                               STANDARD;
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Wong W.T., Kraus M.H., Carlomagno F., Zelano Croce C.M., Huebner K., di Fiore P.P., "The human eps15 gene, encoding a tyrosine k conserved in evolution and maps to 1p31-p32. Oncogene 9:1591-1597(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enmon J.L., de Beer T., Overduin M.;
"Solution structure of Eps15's third I
Phe Trp and Asn-Pro-Phe binding sites
Biochemistry 39:4309-4319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A novel gene, AF-1p, fused related to AF-4, AF-9 nor E Oncogene 9:1039-1045(1994).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98387926; PubMed=9721102;
de Beer T., Carter R.E., Lobel-Rice K.E.,
"Structure and Asn-Pro-Phe binding pocket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               natural target proteins.";
J. Biol. Chem. 271:14468-14472(1996)
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                                                                                                                                                                                                                                                                                                                                                                                          the regulation of mitogenic signals and control of cell proliferation. Involved in the internalization of ligand-inducible receptors of the receptor tyrosine kinase (RTK) type, in particular EGFR (By similarity).
SUBUNIT: Interacts with Stonin 2. Interacts with considering sites.
rogue activator protein.
SIMILARITY: Contains 3 EH domains.
SIMILARITY: Contains 2 EF-hand calcium-binding domains.
SIMILARITY: Contains 2 ubiquitin-interacting motif (UIM) repeat.
DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/AFIpID11.html"
                                                                                                                                         TISSUE SPECIFICITY: Ubiquitously expressed.

PTM: Phosphorylation on Tyr-849 is involved in the internalization of Edgr. Not required for membrane translocation after EGF treatment or for targeting to coated pits, but essential for a subsequent step in EGFR endocycosis (By similarity).

DISEASE: Involved in a t(1;11)(p32;q23) chromosomal translocation in acute leukemias causing fusion to the trithorax (MLL or HRX) gene product which contains DNA-binding motifs resulting in a
                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic. Recruited to the membrane upon EGFR activation and localizes to coate
                                                                                                                                                                                                                                                                                                                                         similarity)
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L; Z29064; CAA823(
; S43074; S43074.
; 1C07; 19-JUL-00.
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                                                                                                                                     WAITVEERAKHDQQFLSLKFIAGFITGDQARNFFFQSGLFQFVLAQIWALADMNNDGRMD
 NTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSL
                                              GSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWPKSSSFSRSGPGSQL
                                                                                                                WAVKPEDKAKYDAIFDSLSPVNGFLSGDKVKPVLLNSKLPVDILGRVWELSDIDHDGMLD
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98673 MW;
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SH3-BINDING.
PHOSPHORYLATION (BY EGFR)
SIMILARITY).
M -> I (IN REF. 2).
M -> I (IN REF. 2).
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                                                                                                                                                            Score 486.5; DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcium-binding; Repeat; oto-oncogene; 3D-structure.
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7e-12;
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                                                                                                                                                            345;
                                                                    -KEPVPM
                                                                                                                                                            Gaps
                       SKR
                                              194
                                                                    203
                                                                                          134
                                                                                                                181
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RESULT 8
EP15 M
EP15 M
AC P42567
DT 01-NOV
DT 15-SEP
DE EP16er
DE PICOE
GN EP515.
GN EP515.
GN EP515.
GN CHARTY
OC Mammall
COX MCB1 T
RN [1]
RP SEQUEN
RC TISSUE
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                                                                                                              EP15 MOUSE
P42567;
01-NOV-1995
01-NOV-1995
15-SEP-2003
                                           Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
SEQUENCE FROM N.A. TISSUE=Fibroblast;
                              NCBI_TaxID=10090;
                                                                                         protein).
                                                                                                   Epidermal
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                                                                                                                                                                                                                                                                                                                                                                                                                          ----AKPEMQDKQSRLFHPHQEPAK-----LATQAPWSTTEKGPLTISAQESV
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                                                                                                   growth
                                                                                                 (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
rowth factor receptor substrate 15
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                                                                                                                                                            STANDARD;
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                                             Chordata;
Rodentia;
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                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KQQLQKQRSLEAARLKQKEQERKSLEL----
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SMART; SM00054; EFh; 4.

SMART; SM00027; EH; 3.

SMART; SM00726; UIM; 3.

PROSITE; PS00018; EF HAND; 2

PROSITE; PS50031; EH; 3.

PROSITE; PS50330; UIM; 2.
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                                                                                                                    DOMAIN
                                                                                                                                                                                                          InterPro; IPR002048; EF-hand.
InterPro; IPR0020261; EPS15_homology.
InterPro; IPR003903; UIM.
Pfam; PF00036; efhand; 4.
                                                                                                                                                                                                                                                                                                                  EMBL; L21768; AAA02912.1; -.
                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                  between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20411232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity.";
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"eps15, a novel tyrosine kinase substrate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93361014; PubMed=7689153;
                                                                                                                                                                                                                                                        ; A54696; A54696.
; 1KYF; 12-JUN-02.
; 1KYU; 12-JUN-02.
; 1QJT; 11-SEP-02.
; MGI:104583; Eps15
                                                                                                                                                                                                                                                                                                                                                                                                                               membrane upon EGFR activation and localizes to coated pits. PTM: PhosphoryLation on Tyr-850 is involved in the internalization of EGFR. Not required for membrane translocation after EGF treatment or for targeting to coated pits, but essential for a subsequent step in EGFR endocytosis.

SIMILARITY: Contains 3 EF domains.

SIMILARITY: Contains 2 EF-hand calcium-binding domains.

SIMILARITY: Contains 2 ubiquitin-interacting motif (UIM) repeats.
                                                                                                                                                                                                                                                                                                                                                                          Buropean Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity). Interacts with Stonin 2.
SUBCELLULAR LOCATION: Cytoplasmic. Recruited to the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  particular EGFR.
SUBUNIT: Interacts with CRK via its SH3-binding sites
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                                                                                                                             3D-structure
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                                                                                                                                                                                                                                                                                                                                                            Usage
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SSNTSVETWGHNDPFAPGGTVVAAASDSATDPFASVFGNESFG-DGFADFSTLSKVNNED
                                                                                                                                                                                                    VOONSLHRDSLLTLKRALEAKELARQQLREQLDEVERE----TRSKLQEIDVFNNQLKE
                                                                                                                                                                                                                          QLQEVRKKCAEEAQLISSLK-----
                                                                                                                                                                                                                                            KLQDIRCRLATORQEIESTNKSRELRIABITHLQQQLQESQQMLGRLIPEKQILSDQLKQ
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                    RALYPFESRSHDEITIQPGDIVMVDESQTGEP--GWLGGELKGKTGWFPANYAEKIPENE
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                                          QSDPFVGSDPFKDDPFGKIDPFGGDPFKGSDPFASDCFFKQTSTDPFTTSSTDPFSASSN
                                                                                        PEIAPSDVTDESEAVTVAGNEKVTPR--FDDDKHSKEEDPFNVESSSLTDAVADTNLDFF
                                                                                                            ER-----DKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKEA----EERAKPEMQDK
                                                                                                                                                                              LQQETAQ----LEESVESGKAQLEPLQQHLQESQQEISSMQMRLEMKDLETDNNQ---
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UIM 2.
PHOSPHORYLATION (BY EGFR).
Y->F: INEFFICIENT EGFR INTERNALIZATION.
MW; OBAOCOD423F873C2 CRC64;
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Pred. No. 4.9e-12;
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P32521;
01-OCT-1993
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MEDLINE=95282515; PubMed=7762303;

Voss H., Tamames J., Teodoru C., Valencia A., Sensen C., Wiemann S.,

Schwager C., Zimmermann J., Sander C., Ansorge W.;

Schwager C., Zimmermann J., Senser C., Ansorge W.;
EMBL; Z38062; CAA86208.1; --
EMBL; X79743; CAB38097.1; --
EMBL; M90688; AAA34841.1; --
PIR; 548440; S48440.
SGD; S0001445; PAN1.
                                                                                                                                                                                                                                                                 PubMed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
Nature 387:84-87(1997).
-i- FUNCTION: NOT KNOWN.
                                                                                      use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=S288C;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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15-SEP-2003
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European Bioinformatics Institute. The by non-profit institutions as long
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SIMILARITY: CONTAINS 2 EH domains.
CAUTION: WAS ORIGINALLY THOUGHT TO
POLY(A)-SPECIFIC RIBONUCLEASE.
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(Rel. 31, Last sequence update)
(Rel. 42, Last annotation update)
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GG; GO:0005886; C:plasma membrane; IDA.
GG; GO:0008093; F:cytcoskeletal adaptor activity; IPI.
GG; GO:0007120; P:axial budding; IMP.
GG; GO:0007128; P:endocytcosis; IMP.
GG; GO:0006897; P:endocytcosis; IMP.
GG; GO:0007121; P:polar budding; IMP.
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SM00027; EH; 7
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                                   ITAQDQAK -> YYCPRSGKN (IN REF. 1).
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A -> R (IN REF. 1).
BGDULFEPTQQASTSEPITAHYDNYNGAEKGTGAYGS
DSDDDVLSIPESVGTDEEEEGAQPVSTAGIPSIPBAGIPP
PPPLP -> EAPCLHPHLYQLNKLPLQNLLSITLITTMVL
KKARAHNDPILMMTFYRFLNQLVQNKRKKGHNQFLLQVSH
                       QFHLQVFLHPHPFHEDLICFL MW; F3518495FF759553 C
Score 410.5; DB 1
Pred. No. 6.1e-09;
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       DB 1;
      Length 1480;
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Matches 261;

Local

Similarity

Conservative

Mismatches

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Gaps

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AEKIPENEVPTP----AKPVTDLTSAPAPKLALRETPAP--LPVTSSEPSTTPNNWADFS
                                            SAS-----STSTFDARAAEMQRRIQRG----LDEDE--DDGWSDEDESNNR----VAV
                                                                                         QESVKVVYYRALYPFESRSHD-EITIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANY
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           PIR; S45781; S45781.

SGD; S0000143; EDE1.
GO; GO:0005887; C:actin cortical patcl
GO; GO:0005893; C:bud neck; IDA.
GO; GO:0005934; C:bud tip; IDA.
GO; GO:0006897; P:endocytosis; IMP.
InterPro; IPR000261; EPS15 homology.
InterPro; IPR000449; UBA_domain.
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YBE7_
                                                                                                                                                                                                                                                                                                                          Scherens B., el Bakkoury M., Vierendeels F., Dubois E., "Sequencing and functional analysis of a 32,560 bp segn left arm of yeast chromosome II. Identification of 26 c frames, including the KIP1 and SEC17 genes."; Yeast 9:1355-1371(1993).

-i- SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
-i- SIMILARITY: Contains 3 EH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 150.8 kDa protein in SEC17-QCR1 intergenic region.
YBL047C OR YBL0520 OR YBL0501.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomyceteles; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of a 22.4 kb DNA fragment from the left chromosome II reveals homologues to bacterial proline murine alpha-adaptin, as well as a new permease and a
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P34216;
                                                                                                                                   EMBL; Z35808; CAA84867.1;
EMBL; X78214; CAA55048.1;
EMBL; Z23261; CAA80797.1;
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S288c;
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Matches 286
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SMART; SM00027; EH; 3.

SMART; SM00165; UBA; 1.

PROSITE; PS50031; EH; 3.

PROSITE; PS50030; UBA; 1.

Hypothetical protein; Repeat.

DOMAIN 135 227

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86; Conservative
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                                                                                                             SKLNE----LTTDLQESQTKNAELKEQITNLNSMTASLQSQLNEKQQ-------
                                                                                                                                          GKLQDIRCRLATQRQEIESTNKSRELRIAEI----THLQQQLQESQQMLGRLIPEKQILS
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                         LREIHSKQQLQKQRSLEAARLKQKEQE--RKSLEL---EKQKEDAQRRVQERDKQWLEHV 663
                                                                                                                                                                      KLNNLRSTHDQNVKQTEQLEAQVL - - QVNKENE-
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                                                                                                                                                                     -----TLAQQLAVSEANYHAAE
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                                                       -EKISVYLTKQKE
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01-OCT-1994
15-SEP-2003
                                                                                                                         Fietz M.J., ROGETS G.E.;

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES

-IN REGILAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIERPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN LITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRHY RABIT P37709;
                                                                                                                                                                                                                                                                                                                                                                                                                             THH.
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                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9986
                                                                                                                                                                                                                                                                                                                                                                                                                                             Trichohyaiin
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SUBUNIT: Homodimer (Probable).

TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES S THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, A THE FILLFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE) DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OTHE EPIDERMIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVFDRDVPTLGSQSDSENANTNNGTQSGNETANP-NLTETLSDRFDGDLNEYGIPRSQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---VRKSTSIDTGPTESPASIKRVASPAAKPAIP--GEEFIAMYTYESSEQGDLTFQQGD
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InterPro;

R InterPro; IPR002046; 1.

R Pfam; PP00036; efhand; 1.

DR Pfam; PP01023; S 100; 1.

DR ProDom; PD003407; CaBP_S100; 1.

DR PROSITE; PS000103; SITO CABP; 1.

DR PROSITE; PS000103; SITO CABP; 1.

W Keratinization; Calcium-binding; Repeat; Citrullination.

KW Keratinization; 2 33 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).

TOMAIN 2 33 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

TOMAIN 2 33 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

ABITODAN159F12B7F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P02633; 4ICB.
InterPro; IPR001751; CaBP
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DIFFERENT SPECIES.

TO TRANSCLUTAMINASE. SOME 200 ARGININES ARE PETM: SUBSTRATE OF TRANSCLUTAMINASE. BY PEPTIDYLARGININE DEIM:

OFFICIAL CONTAINS OF THE S-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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L---KREDSVRKKEAEERAKPEMQ
                                                                        LQREKRRQ-EREREYREEEKLQREEDEKKRRQERERQYRELEELRQEEQLRDRKLREEEQ
                                                                                                                                                                                 RAQQLQEEDSFQEDRERRRQQEQRPGQTWRWQLQEEAQRRRHTLYAKPGQQEQLREEEE
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                                                                                                                              LEAARLKQKEQERKSLELEK--QKEDAQRRVQERDKQW--LEHVQQEEQPRPRKPHEEDR
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29.7%;
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Pred. No. 3.
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C: -! SUBUNIT: MONOMER (Probable).

C: THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND MEDULLA, AND IN

THE FILIFORM PAPILLAE OF DORSAL TONGUE BUTTHELIUM (PROBABLE).

C: -! DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF

C: -! DOWALLOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF

C: -! DOWALN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND

CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST

CALCIUM-BINDING DOMAINS. DOMAINS 2-7, 6, AND 8 ARE ALMOST

CENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REBEATS

C: OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED

C: ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS

C: THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS.

C: THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS.

C: THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS.

C: THE MOST REGULAR. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
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01-OCT-1994
15-SEP-2003
                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1731-1898 FROM N.A., AND CHARACTERIZATION MEDILINE=93315897; PubMed=7686953; O'Keefe E.J., Hamilton E.H., Lee S.-C., Steinert P.M. "Trichohyalin: a structural protein of hair, tongue, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   envelope precursor, and an intermediate linking) protein.";
J. Biol. Chem. 268:12164-1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epidermis."
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Mammalia; Eutheria; Primates;
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THH OR TRHY OR THL.
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                 EMBL; L09190;
                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=93280194; PubMed=7685034;
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                                                                                                                                                                                                                                            DIFFERENT SPECIES.

PTM: SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                         SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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Metazoa; C
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                   AAA65582.1;
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pfam; PF01023; S 100; 1.
proDom; PD003407; CaBP S100; 1.
pROSITE; PS00018; EF HAND; 1.
pROSITE; PS00303; S100_CABP; 1.
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InterPro; IPR001751; CaBP S100.
InterPro; IPR002048; EF-hand.
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GO:0005856; C:cytoskeleton; NAS.
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QERDRQYR -> RSETGSTG (IN REF ^^
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P22793;
01-AUG-1991
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-:- FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THI INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIFEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK.
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Mammalia; Eutheria;
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1016-1549 FROM N.A.
ISOID-P22793-2; Sequence=VSP 000847, VSP 000848; TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING THE INNER ROOT SHEATH (IRS) OF HAIR FOLLICLES AND M THE EPITHELIA OF THE TONGUE, HOOF AND RUMEN.

DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE RE
                                                                                                                                                                             SUBUNIT: Homodimer (PALTERNATIVE PRODUCTS:
                                                                                                        Name=Short;
                                                                                                                                     Name=Long;
                                                                                                                                                 Event=Alternative splicing; Named Comment=Additional isoforms seem
                                                                                                                                                                                                             DIFFERENTIATION
                                                                                                                                                                                                                          ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC
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                                                                                                                    IsoId=P22793-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence up
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                                                                                                                                                                                              (Probable).
                                                                                                                                                                                                                                                                                                                                                                       cid sequence for trichohyalin, the hair follicle, contains a
                                                                                                                                                   seem
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   DOMAIN 1 CONTAINS TWO EF-HAND
2-4, 6, AND 8 ARE ALMOST ENTIRE
RIES OF PEPTIDE REPEATS OF
                                                                                                                                                 isoforms=2;
m to exist;
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the hair follicle.";
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ProDom; PD003407; CaBF S100; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00303; S100_CABF; FALSE_NEG.
Keratinization; Calcium-binding; Repeat; Citrullination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z18361; CAA79165.1; -.
EMBL; X51695; CAA35992.1; -.
PIR; A40691; A40691.
                                                                                                                                        REPEAT
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InterPro; IPR002048; EF hand.
Pfam; PF00036; efhand; 1.
Pfam; PF01023; S_100; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P02633; 1IG5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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PTM: SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 2 EF-hand calcium-binding domains
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EF-HAND 2 (HIGH AFFINITY) (POTENTIAL)
14 X 28 AA APPROXIMATE TANDEM REPEATS
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                     Humphrey M.B., Herrera-
"Cloning of cDNAs encod
Gene 112:197-204(1992).
                                                                                                                             Novy R.E., Lin J.L.-C., Lin J.J.-C.; "Characterization of cDNA clones encoding a human fibroblast caldesmon isoform and analysis of caldesmon expression in no
                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 4).
TISSUE=Lung fibroblast;
MEDLINE=91358497; PubMed=1885618;
                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                             Caldesmon (CDM).
CALD1 OR CDM OR CAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                          MEDLINE=92209999; PubMed=1555769;
                                                                                                                                                                                                              NCBI_TaxID=9606;
SEQUENCE FROM N.A.
                                                                                 SEQUENCE FROM N.A.
                                                                                                                     transformed cell
                                                                                                         Biol.
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                                                                                                         Chem. 266:16917-16924(1991).
                                                                                                                                                                                                                                                                                                                                                                                                               RVQERDKQWL--EHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEER--AKPEMQDKQSRL
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/FTIId=VSP 000847.
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/FTIId=VSP 000848.
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Catarrhini; Hominidae;
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1 caldesmons.
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EMBL; M64110; AAA35636.1; --
EMBL; M83216; AAA58420.1; --
EMBL; M83216; AAA58419.1; --
EMBL; D80452; BAA14418.1; --
EMBL; D90453; BAA14419.1; --
PIR; JH0628; JH0628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                            Genew; HGNC:1441; GK; Q05682; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a or send an email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi E.-I., Kato I., Sobue K. "Genomic structure of the human ca
                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi
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                                                                         nterPro;
GO:0005856; C:cytoskeleton; TAS.
GO:0003779; F:actin binding activity; TAS.
GO:0005516; F:calmodulin binding activity; TAS.
GO:0005523; F:tropomyosin binding activity; TAS.
GO:0005523; F:tropomyosin binding activity; TAS.
erPro; IPR0060117; Caldesmon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: THE N-TERMINAL PART SEEMS TO BE A MYOSIN/CALMODULIN-BINDING DOMAIN, AND THE C-TERMINAL A TROPOMYOSIN/ACTIN/CALMODULIN-BINDING DOMAIN. THESE TWO DOMAINS ARE SEPARATED BY A CENTRAL HELICAL REGION IN THE SMOOTH-MUSCLE FORM.

PTM: IN NON-MUSCLE CELLS, PHOSPHORYLATION BY CDC2 DURING MITOSIS CAUDESMON TO DISSOCIATE FROM MICROFILAMENTS.
PHOSPHORYLATION REDUCES CALDESMON BINDING TO ACTIN, MYOSIN, AND CALMODULIN AS WELL AS ITS INHIBITION OF ACTOMYOSIN ATPASE ACTIVITY. PHOSPHORYLATION ALSO OCCURS IN BOTH QUIESCENT AND DIVIDING SMOOTH MUSCLE CELLS WITH SIMILAR EFFECTS ON THE INTERACTION WITH ACTIN AND CALMODULIN AND ON MICROFILAMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. NATI. ACAD. SCI. U.S.A. 89:12122-12126(1992).

TUNCTION: ACTIN- AND MYOSIN BINDING PROTEIN IMPLICATED IN THE REGULATION OF ACTOMYOSIN INTERACTIONS IN SMOOTH MUSCLE AND NONMUSCLE CELLS (COULD ACT AS A BRIDGE BETWEEN MYOSIN WHICH INCREASES THE STABILIZATION OF ACTIN FILAMENT STRUCTURE. IN MUSC TISSUES, INHIBITS THE ACTOMYOSIN ATPASE BY BINDING TO FACTIN. THIS INHIBITS THE ACTOMYOSIN ATPASE BY BINDING TO FACTIN. THIS INHIBITION IS ATTENUATED BY CALCIUM-CALMODULIN AND IS POTENTIATED BY TROPOMYOSIN, INTERACTS WITH ACTIN, MYOSIN, TWO MOLECULES OF TROPOMYOSIN AND WITH CALMODULIN. ALSO PLAY AN ESSENTIAL ROLE DURING CELLULAR MITOSIS AND RECEPTOR CAPPING. SUBCELLULAR LOCATIONS ON THIN FILAMENTS IN SMOOTH MUSCLE AND ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q05682-5; Sequence=VSP 004154, VSP_004156; TISSUE SPECIFICITY: High-molecular-weight Caldesmon (isoform 1) in predominantly expressed in smooth muscles, whereas low-molecular-weight caldesmon (isoforms 2, 3, 4 and 5) are widely distributed in non-muscle tissues and cells. Not expressed in skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REORGANIZATION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CALDESMON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q05682-3; Sequence=VSP 004154,
Name=4; Synonyms=WI-38 L-CAD II, 1-CAD;
IsoId=Q05682-4; Sequence=VSP 004156;
Name=5; Synonyms=HELA L-CAD II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1; Synonyms=H-CAD;
IsoId=Q05682-1; Sequence=Displayed;
Name=2; Synonyms=WI-38 L-CAD I;
IsoId=Q05682-2; Sequence=VSP 004155;
Name=3; Synonyms=HELA L-CAD I;
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or heart.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 equires a license agreement (S
email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yano H., Hashida T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions ng as its content is in
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FEKLKOKOOE-AALELEELKKKREERRKVLEEEEO--RRKOEEADRKLREEEEKRRLKEE
                                                                                                                            ELEALNDKKHQLEGKLQDIRCRLATQRQEIES-----TNKSRELRIAEITHLQQQLQES
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                AARLKQKEQERKSLELE--KQKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDRLKRE
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                                   VKSQNGEFMTHKLKHTENTFSRPGGRASVDTKEAEGAPQVEAGKRLEELRRRRGETESEE
                                                     SKLOEIDVFNNQLKELREIHSK----
                                                                                         QQMLGRLIPEKQILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETR
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CALMODULIN-BINDING (BY SIMILARITY).
WEAK ACTIN-BINDING (BY SIMILARITY).
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                        Missing (i
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POLY-ARG.
POLY-GLU.
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                                                                                                                                                                                                                                                                                                                    Missing (In isoform /FTId=VSP_004156.
                                                                                                                                                                                                                                                                                                                                                          MDDFERRRELRROKREEMRLEAER -> MLGGSGSHGRRSL
AALSQ (in isoform 3 and isoform 5).
/FTId=VSP_004154.
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15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mitogen-activated protein kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase
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   serine/threonine kinase
Submitted (APR-1998) to
                                                                                                                                                                                                                                                       Duesterhoeft A., Lauber
Submitted (JAN-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka Kotani H., Nomura N., Ohara O.; Rodinton of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=12612079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Glioblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yao Z., Zhou G., Wang X.S., Brown A., Diener K., Gan H., Tan T.-H.; "A novel human STE20-related protein kinase, HGK, that specifically activates the c-Unu N-terminal kinase signaling pathway."; J. Biol. Chem. 274:2118-2125(1999).
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MEDLINE=99107863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; V. Mammalia; Eutheria; Primates; Catarrhini;
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   "Isolation, expression profile and chromosome assignment serine/threonine kinase gene.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98403880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 23:2068-2082(2003).
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                                                                                                                                                                                                                                                                                                                                                                  OF 262-1239 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                     large proteins in vitro."; 5:169-176(1998).
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                                                                                                              Seki N., Hori T.;
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SIMILARITY).

(in isoform 5).

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isoform

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and

DOMAIN

DOMAIN Alternative ATP-binding;

PROTEIN CNH.

KINASE

InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00780; CNH; 1.
Pfam; PF000669; pkinase; 1.
Propom; PD000001; Prot_kinase; 1.

SMART; SM00036; CNH; 1. SMART; SM00220; S_TKC; 1. SMART; SM00219; TYrKC; 1.

PROSITE; PS00107; PROSITE; PS50011; PROSITE; PS00108;

PROTEIN_KINASE_ATP; PROTEIN_KINASE_ST;

- -

Serine/threonine-protein

kinase;

Transferase,

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This SWISS-PROT entry is copyright. It is produced the EMBL of Bioinformatics and the EMBL of Bronzen the Swiss Institute of Bioinformatics are no restrict the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed. Usage by and formodified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                          MIM; 604666; -.

GO; GO:0005524; F:ATP binding; IDA.

GO; GO:0004674; F:protein serine/threonine kinase; IDA

GO; GO:000468; P:protein amino acid phosphorylation;

GO; GO:0007243; P:protein kinase cascade; IDA.

GO; GO:0007165; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                               InterPro; IPR001180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Serine/threonine kinase that may play a role in the response to environmental stress and cycokines such as TNF-alpha. Appears to act upstream of the c-jun N-tearminal pathway. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. COFACTOR: Magnesium.
SUBUNIT: Interacts with the SH3 domain of the adapter proteins NCK (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=095819-5; Sequence=VSP_007054, VSP_007055, VSP_007056

VSP_007057, VSP_007058;

TISSUE SPECIFICITY: Appears to be ubiquitous, expressed in al tissue types examined. Isoform 5 appears to be more abundant the brain, isoform 4 is predominant in the liver, skeletal muthe brain, isoform 4 is predominant in the liver, skeletal muther brain, isoform 4 is predominant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 1 CNH domain.
CAUTION: Ref.4 sequence differs from that shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frameshift in position 1151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STE20 SUBFAMILY
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AB013385; BAA33714.1; -.
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AL137755;
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IsoId=095819-5; Seque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=095819-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:6866; MAP4K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :soId=095819-3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         =095819-3; Sequence=VSP_007056,
Synonyms=HGK-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synonyms=Tumor-associated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO32626.1;
BAA31662.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD16137.1; -.
                                                                                                                                                                                                                                                                                                                  Citron
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	566	9 LKQKEQERKSLELEKQKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRK : ::	629 514	₽ ₹
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	39;	h 5.3%; Score 330; DB 1; Length 1239; Similarity 22.1%; Pred. No. 6e-06; 93; Conservative 116; Mismatches 222; Indels 342; Gaps	Query Match Best Local Matches 19	~ ~
		658 .658 839 839 1239 AA; 142100 M	CONFLICT CONFLICT SEQUENCE	0111
		/FTId=USP 007057. C 1112 1112 H -> HVRKNPHSM (in isoform 4 and isoform 5).	VARSPLI	444
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Search completed: December 4, 2003, 15:19:11 Job time : 22 secs

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ALIGNMENTS

Query Match 68.0%; Score	SEQUENCE 1220 AA; 136351 MW;	DR PROSITE; PS50002; SH3; 5.	PROSITE; PS50031;	PROSITE; PS00018	M00326; SH	SMART; SM00027;	DR SMART; SM00054; EFh; 2.	ProDom;	DR PRINTS; PR00452; SH3DOMAIN.	Pfam; PF00036; efhanc	<pre>InterPro; IPR001452;</pre>	InterPro; IPR000108; Neu_c	<pre>DR InterPro; IPR000261; EPS15_homology.</pre>	InterPro; IPR002	DR EMBL; AL606751; CAD43427.1;	-!- SIMILARITY: CONTAINS 5 S	RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ	Pandian R	RP SEQUENCE FROM N.A.	OX NCBI_TaxID=7955;	Cyprinidae; Danio.	Actinopterygii; Neopterygii;	Eukaryota; Metazoa; Chordata;	Brachydanio rerio (Zebrafish)	protein, ITSN1)).	SI:dZ173A8.1.2 (Novel protein si	01-MAR-2003 (TrEMBLrel. 23, Last	01-OCT-2002 (TrEMBLrel. 22, Last	01-OCT-2002 (TrEMBLrel.	Q8JFT5;	ID Q8JFT5 PRELIMINARY; PRT;	Q8UFT5
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                                                                                                                                                                                                                                                                                                                                       ELERORESERKEIERREAAKRELEROROLEWERTRROELLTORNREGENIVLLKARKKT
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                                                                                                                                                                                                                                                                                                                                                                                                                    FERGNLELEKRROALLEOORKEOERLAALEKEEOERKERERLEOERRROOELDKOLEROR
                                                                                                                                                                                                                                                                                                                                                                                                                                 FERGSVELEKRRQALLEQQRKEQERLAQLERAEQERKERERQEQEAKRQLELEKQLEXQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILPPDLIPTFRRMRSGSGVSVTSMHSTDLRSQEEP-EEEEKEAEKKLPVTFEDKKREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVLPPEYIPPSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQQPEKKLPVTFEDKKREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKTPSFNRS-----SIKLQKGQSVEAPSAPAAPPPADWAVSQSSRLKYRQLFNSHDKMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKSSSFSRSGPGSQLNTKLQKAQSFDVAS---APPAAEWAVPQSSRLKYRQLFNSHDKTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SIPP----PTPFG-VPGMGVSPPLGASVTP-PVPSLANGAPAMIQPLSGFSHPGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WRAKKDNHLNFNKNDVITVLEQQDMWWFGEVQGQRGWFPKSYVKLISGPVRKSMSIDSGS
                                         WRAKKDNHLNFNKSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGP
                                                                    SDGWDAWPTQPTQPSLSVPSGGQIRQRSAFTPATLSGSSPSPVLGQGEKVEGLQAQALYP
                                                                             TDNWDTW----AAQPSLTVPSAGQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYP
                                                                                                                                                                                    RVNVRNQHKSCVC-----VLDKIPVSGFNQEKVKVVYYRAMYPFEARSHDEITIHPGDI
                                                                                                                                                                                                                         ---LSGTDDGVSPAWRDDGLGKAPTPPVSQAWMSR----VREKKIVDAERHGFDQFCCCFM
                                                                                                                                                                                                                                                               LEIDAFNTQLKELREIHNKQQRQKQKELE-ADITQPSHDRKSIDSQDSR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGYLTGPQARTILMQSSLPQAQLATIWNLSDIDQDGKLTAEEFILAMHLIDMAMSGLPLP
                                                                                                                   -----APKLALRETPAPL-PVTSSEPSTTP-----NNWADFSSTWPSSSN-EKPE
                                                                                                                                                VMVDES
                                                                                                                                               OTGEPGWLGGEIKGKTGWFPANYAEKIPESEVPLSLRASAASSSAPKLGSHMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.5e-206;
8; Mismatches 184;
-IPGEEFIAMYTYESSEQGDLTFQQGDVIV
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  Query Match
Best Local
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  Similarity
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밁
                   Pfam; PF00168; C2; 1.
Pfam; PF00169; efhand; 2.
Pfam; PF00169; pH; 1.
Pfam; PF00169; pH; 1.
Pfam; PF00621; RhoGEF; 1.
PFAMTS; PR00499; P67PHOX.
PRINTS; PR00499; C2; 1.
SMART; SM000259; C2; 1.
SMART; SM000239; C2; 1.
SMART; SM00027; EH; 2.
SMART; SM000325; RhoGEF; 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00325; SH3; 5.
PROSITE; PS50004; C2 DOMAIN_2; 1.
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50011; EF; HAND; 2.
PROSITE; PS50013; PH DOMAIN; 1.
PROSITE; PS50013; PH DOMAIN; 1.
PROSITE; PS50003; PH DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8JFT4 PRELIMINARY; FKI; 1/21 cm.
Q8JFT4;
Q1-CT-2002 (TrEMBLrel. 22, Created)
Q1-CCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SI:dZ173A8.1.1 (Novel protein similar to intersectin (SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 PH DOWAIN.
-!- SIMILARITY: CONTAINS 5 SH3 DOMAINS.
-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
EMBL; AL606751; CAD43428.1; -.
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SI:DZ173A8.1.
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InterPro; IPR002048; EF hand.
InterPro; IPR000261; EFS15_homolo;
InterPro; IPR000108; Neu_cyt_fact.
InterPro; IPR001849; PH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000219;
InterPro; IPR001452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
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AA;
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194115 MW;
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2E57E7895E4D9C07 CRC64;
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68.0**%**;

Score 4264.5; DB 1 Pred. No. 2.3e-206;

13;

Length

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Matches
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                                                                                                                                                                                                                                                                                                                                                          RLFHPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGHLTGPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKPI-AGFITGDQARNFFFQSGLPQPVLA
                                                                                                                                                      VMVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAP------
                                                                                                                                                                                                                                                                                                                                                                                                           ---LSGTDDGVSPAWRDDGLGKAPTPPVSQAWMSR---VREKKIVDAERHGFDQFCCCFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEIDVFNNQLKELREIHSKQQLQKQRSLEAARLKQKEQERKSLELEKQKEDAQRRVQERD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGRLIPEKQILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEFELEALNDKKSQLEGKLQDIRSRLSIQRHEIETTNKTRELRIAEITSLQQQLQESQQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELERORESERRKEIERREAAKRELEROROLEWERTRROELLTORNREGENIVLLKARKKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKTPSFNRS----SIKLQKGQSVEAPSAPAAPPPADWAVSQSSRLKYRQLFNSHDKMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAQFPTPFGGGSDTWVISVDERAKHDQQFHSLTPTPAGFITGDQARNFFLQSGLPAPILA
SDSPPSVKRPSPSLNKPTELGEGQNSNSNSMYPSKEYVAMYTYESNEQGDLTFQQGDVIT
                 WRAKKONHLNENKNOVITVLEQQOMWWFGEVQGQRGWFPKSYVKLISGP
                                                                                       WRAKKDNHLNENKSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISGFVRKSTSIDTGF
                                                                                                                                 SDGWDAWPTQPTQPSLSVPSGGQIRQRSAFTPATLSGSSPSPVLGQGEKVEGLQAQALYP
                                                                                                                                                                                                                      ----APKLALRETPAPL-PVTSSEPSTTP-----NNWADFSSTWPSSSN-EKPE
                                                                                                                                                                                                                                                                                                                                          RVNVRNQHKSCVC-----VLDKIPVSGFNQEKVKVVYYRAMYPFEARSHDEITIHPGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEIDAFNTQLKELREIHNKQQRQKQKELE-ADITQPSHDRKSIDSQDSR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FERGNLELEKRRQALLEQORKEQERLAALEKEEQERKERERLEQERRRQQELDKQLERQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGYLTGPQARTILMQSSLPQAQLATIWNLSDIDQDGKLTAEEFILAMHLIDMAMSGLPLP
                                                                                                                                                                                                   ASSSTTATPILPVSTEPASIAPPSSAPPPTGPASSSSSASSNWADFSTTWPSNSAVEKQD
                                                                                                                                                                                                                                                                      VMVDESQTGEPGWLGGE1KGKTGWFPANYAEK1PESEVPLSLRASAASSSAPKLGSHMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ------RPRKPHEEDRLKREDSVRKK---EAEERAKPEMQDKQS
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                                                               VRKSMSIDSGS
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addams M.D., Celniker S.E., Holt R.A., Howkins R.A., Galle R.F., RA Addams M.D., Celniker S.E., Holt R.A., Howkins R.A., Galle R.F., RA Addams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D., RA George R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D., RA Burtis K.C., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier R., RA Gerry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P., RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. RA Goldson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. RA Goldson K., Doug I.E., Downes M., Dugan-Rocha S., Pleischmann W., RA Harris N.I., Harvey D., Heiman T.J., Hermandez J.R., Houck J., RA Harris N.I., Harvey D., Heiman T.J., Hermandez J.R., Houck J., Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kilp D., Lai Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshinan N.V., Mobarry C., Morris J., Moshrefi A., Rount S.M., Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L., RA Merlandov G.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Merlandov G.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Merlandov G.M., Milshinan N.V., Mobarry C., Morris J., Moshrefi A., Ra Melson D.R., Nelson K.A., Winskern D.R., Pacleb J.M., Nelson D.L., Ra Allein M., Wolley K.C., Wu D., Yang S., Yao Q.A., Ye J., RA Mang Z.Y., Massarman D.A., Weinstock G.M., Weissenbach J., Ra Syirskas R., Terctor C., Zhang M., Zhang G., Zhang
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Adams M.D., Celnil
Amanatides P.G.,
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Eukaryota; Metazoa; Arthropoda; Hexaspoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                  Smith H.O.,
                                                                                                                                                                              Үе J.,
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RP SEQUENCE FROM N.A.

RA Celniker S.E., Adams M.D., Kronmiller B., wa....

RA Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Avy-Ra Carlaen J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

"Sequencing of Drosophila melanogaster genome.",

PI. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A., Matthews B.B., Bayraktaroglu L., Campbell K.

Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,

Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,

Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,

"Annotation of Drosophila melanogaster genome.";

submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2002)
EMBL; AE003669; AAN11
SEQUENCE 1014 AA;
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NCE 1014 AA; 111890
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D., Celniker
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KORELEROREEERKEIERREAAKRELEROROLEWERNRROELLNORNKEOEGTVVLKAR
                                                               RENFERGSVELEKRROALLEQQRKEQERLAQLERAEQERKERERQEQEAKRQLELEKQLE
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                                                                                                                                                                                                                  SGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQART
                                                                                                                                                                                                                                                         SLSPLD---
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                                          KENYVKGQAELDRRRKIMEDQQRKEREERERKEREEADKREKARLEAERKQQEELERQLQ
                                                                                                                       FRRVRSGSGMSVISSSSVDQRLPEEPSSED-----EQQPEKKLP--VTFEDKK
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larity 33.5%;
Conservative 20
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                                                                                            SVSGVVSRPGSQPASRHASVSSQSGVGVVDADPTAGLPGQTSFEDKR
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e EMBL/GenBank/DDBJ
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Pred. No. 1.7e
04; Mismatches
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                                                                                    QQDMWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVASPAAKPAIPG
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                                 AFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSNYV 1202
                                                                                                                                                                                TAAABPVESLDQGMRAKRSEIAQVIAPYEATSTEQLSLTRGQLIMIRKKTDSGWWEGELQ
                                                                                                                                                                                                                TAG-----KTGSLGKKPEIAQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWEGELQ
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D 061639 PRELIMINARY; PRT; 1011 AA.

C 061639; PRELIMINARY; PRT; 1011 AA.

O1-AUG-1998 (TrEMBLrel. 07, Created)

T 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

T 01-AUG-1998 (TrEMBLrel. 23, Last annotation update)

T 01-AUG-1998 (TrEMBLrel. 23, Last annotation update)

Dynamin associated protein isoform DAP160-2.

B Dynamin associated protein isoform DAP160-2.

N DAP160 OR CG1099.

N DAP160 OR CG109
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Query Match
Best Local S
Matches 413
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SMART; SM00027; EH; 2.
SMART; SM000326; SH3; 4.
PROSITE; PS00018; EF HAND; 2
PROSITE; PS50031; EH; 2.
PROSITE; PS50002; SH3; 4.
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InterPro; IPR000261; EPS15_homology.
InterPro; IPR001452; SH3.
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                                             NETSVSSAWDT----
                                                                                        SLELEKOKEDAORRVQERDKOWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEERAKP
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                                                                                                                                                                                                                                                                                                   QQMLGRLIPEK----
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                                             -GSSSAW----
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2; Mismatches
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Pred. No. 2
                                                                                                                                                                                                                                                                                                   -QILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLR
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                                           -EETGTTVTDPY--
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pfam; PF00036; efhand; 2.
Pfam; PF00018; SH3; 4.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 4.
SMART; SM00027; EH; 2.
SMART; SM00027; EH; 2.
SMART; SM00326; SH3; 4.
PROSITE; PS00018; EF HAND; 2.
PROSITE; PS50001; EF; 2.
PROSITE; PS50001; EH; 2.
PROSITE; PS50002; SH3; 4.
Calcium; Calcium-binding; SH3 domain.
SEQUENCE 1097 AA; 120766 MW; 2573D7
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                                                  KENYVKGQAELDRRRKIMEDQQRKEREERERKEREEADKREKARLEAERKQQEELERQLQ
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KQRELERQREEERRKEIERREAAKRELERQRQLEWERNRRQELLNQRNKEQEGTVVLKAR
                                                                                                    RENFERGSVELEKRROALLEQORKEQERLAQUERAEQERKERERQEQEAKROLELEKOLE
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                                                                                                                                                            -SVSGVVSRPGSQPASRHASVSSQSGVGVVDADPTAGLPGQTSFEDKR
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OG1618

PRELIMINARY; PRT; 1094 AA.

OG1618

PRELIMINARY; PRT; 1094 AA.

AC OG1618;

POT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DT 01-MAR-2003 (TrEMBLrel. 1 isoform DAP160-1.

BY Dynamin associated protein isoform DAP160-1.

GN DAP160 OR CG1099.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
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Best Local Similarity
Matches 417; Conserv
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PRODOM; PD000066; SH3; 4.
SWART; SM00054; EPh; 2.
SWART; SM00027; EH; 2.
SWART; SM000326; SH3; 4.
PROSITE; PS00018; EF HAND; 2
PROSITE; PS50002; SH3; 4.
PROSITE; PS50002; SH3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROOS J., Kelly R.B.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 4 SH3 DOMAINS.
EMBL; AF053957; AAC39138.1; -.
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InterPro; IPR002048; EF-hand.
InterPro; IPR000261; EPS15_homology.
InterPro; IPR001452; SH3.
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HSSP; P29354; 1GRI.
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                                                                                                               NTQLNVELSTLNEKIKELSQRICDTRAGVTNVKTVIDGMRTQRDTSMSEMSQLKARIKEQ
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                                                                                                                                                                                                                                                                                                                                              VLVQSKLPQVTLAQIWTLSDIDGDGRLNCDEFILAMFLCEKAMAGEKIPVTLPQEWVPPN
DKVENISKEIESKKEDINTNDVOMSELKAELSALITKCEDLYKEYDVORTSVLELKYNRK
                          EQLDEVERETRSKLQEIDVFNNQLKELRE----IHSKQQLQKQRSLEAARLKQKEQERK
                                                                                 QQMLGRLIPEK------QILSDQLKQVQQNSLHRDSLLTLKRALEAKELARQQLR
                                                                                                                                          RKTLEFELEALNDKKHQLEGKLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQES
                                                                                                                                                                      RQREIEMEKEEQRKRELEAKEAARKELEKQRQQEWEQARIAEMNAQKEREQERVLKQKAH
                                                                                                                                                                                                                              KENYVKGQAELDRRRKIMEDQQRKEREERERKEREEADKREKARLEAERKQQEELERQLQ
                                                                                                                                                                                                                                                                                                                                                                                                     --PPSRHTSISERAPSIESVN---QGEWAVQAAQKRKYTQVFNANDRTRSGYLTGSQARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1094 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 201; Mismatches 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120495 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.1%; Score 1698.5; DB 5; 31.6%; Pred. No. 1.9e-77;
                                                                                                                                                                                                                                                                                     -SVSGVVSRPGSQPASRHASVSSQSGVGVVDADPTAGLPGQTSFEDKR
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RESULT 7
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AC Q81W
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Q8IWH9;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to intersectin 1 (SH3 domain protein) (Fragment).
                                                                                                                                   Strausberg R.;
Submitted (NOV-2002) to the
EMBL; BC039036; AAH39036.1;
NON TER 345 345
SEQUENCE 345 AA; 37077 MP
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                        TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1058
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      328;
                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYYIAAYPYESABEGDLSFSAGEMVMVIKKEGEWWTGTIGSRTGMFPSNYVQKADVGTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEFIAMYTYESSEQGDLTFQQGDVIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTEQILDKVIALYPYKAQNDDELSFDKDDIISVLGRDEPEWWRGELNGLSGLFPSNYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDTEVSQINTQSKTQSSEPAESYSRPMSRTSSMTPGMRAKRSEIAQVIAPYEATSTEQLS: 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAAEPVESLDQETTLNGNAAYTAAPVEAQEQVYQPLPVQEPSEQPISSPGVGAEEAHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTRGQLIMIRKKTDSGWWEGELQAKGRRRQIGWFPATYVKVLQGGRNSGRNTPVSGSRIE
   26.9%;
nilarity 95.3%;
Conservative
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                                                                                                                                          37077 MW;
                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
      9
   Score 1684; DB 4;
Pred. No. 2.5e-77;
5; Mismatches 10;
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                                                                                                                                      CRC64;
                                                                 Length 345;
      Indels
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Q8IWI5;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (NOV-2002) to the
EMBL; BC038963; AAH38963.1;
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YIPPSFRRVRSGSGMSVISSSSVDQRLPEEPSSEDEQQPEXKLPVTFEDKKRENFERGSV
                                                              FQARNALLQSNLSQTQLATIWTLADIDGDGQLKAEEFILAMHLTDMAKAGQPLPLTLPPE
                                                                                                             PQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPVLPPE
                                                                                                                                                                                  THRAPLSSPVPNSSTSSTASLSGNSPKTGTSEWAVPQPTRLKYRQKFNTLDKSMSGYLSG
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Q9U2T9;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00036; efhand; 2. Pfam; PF00018; SH3; 5. PRINTS; PR00452; SH3DOMAIN. ProDom; PD000066; SH3; 5.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                        SH3 domain.
                                                                                                                                                                                                                                         PROSITE; PS00152; ATPASE ALPHA_BETA; PROSITE; PS00018; EF HAND; 2. PROSITE; PS50031; EH; 2. PROSITE; PS50002; SH3; 5.
                                                                                                                                                                                                                                                                                                                                           SMART; SM00027; EH; 2.
SMART; SM00326; SH3; 5
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InterPro; IPR000261; EPS1
InterPro; IPR001452; SH3.
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WormPep; Y116A8C.36; CE23342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998)
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Y116A8C.36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99069613; PubMed=9851916;
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hes 369;
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                                          WAITVEERAKHDQQFLSLKPIAGFITGDQ-----ARNFFFQSGLPQPVLAQIWALADM 67
  WEVSDAEYQKNFAMF-----GQLTGGQPFMDAVTARNALMRSNLPTQVLSQIWALSDL
                                                                                                                                                                                               1097 AA; 122072 MW;
                                                                                               21.3%; Sc
29.4%; Pr
tive 200;
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EPS15_homology.
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Last annotation update)
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                                                                                               Score 1333; DB 5;
Pred. No. 4.8e-59;
0; Mismatches 454
                                                                                                                                                                                               1C2BA5F103968372 CRC64;
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                                                                                                                                               DB 5;
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PGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTELPKTAVQPA 1149
                                                              RCNGREGIFPANYVEISVQQAGDPTPPTQAPTPAAPPTVLCEAKVVVDFVASAPNQLGIK
                                                                                                                            TVGDKSGVFPSNYVRLKDSEGSGTAGKT--GSLGKKPEI---AQVIASYAATGPEQLTLA
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                                                                                                                                                                                                 AGAQYDVVPSDVTLQASETAPQQQLYTVIYDFEAVETTDLALHVGDTILVLEKNDEWWKG
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                                                        Q8C9C3 PRELIMINARY; PRT;
Q8C9C3;
Q8C9C3;
Q8C9C3;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sec
Q1-MAR-2003 (TrEMBLrel. 23, Last and
SH3 domain protein 1B (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cranic
Mammalia; Eutheria; Rodentia; Sciure
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Q8C4B5;
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"Analysis of the mouse transcriptome based on
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK082606; BAC38546.1; -.
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STRAIN-C57BL/6J; TISSUE=Cerebellum;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
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                                             NCBI_TaxID=10090;
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ilarity 99.6%;
Conservative
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Rodentia;
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Pred. No. 2.7e-58;
                                                                            Craniata;
                                                             Sciurognathi;
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Q8CJ43;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                           SEQUENCE
                                                                                                                             "Nover br-
transcripts.";
                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BALB/cxC57BLF1; TISSUE-Lung;
Skripkina I.Ya., Tsyba L.A., Slavov
"Novel splicing forms of human and n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK042449; BAC31264.1; -.
NON TER 440 440
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Nature 420:563-573(2002).
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the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
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                                                                                                           AAN75695.1;
                                                                                                                                    74:33-43 (2002) .
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13.1%;
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Last annotation updat
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Pred. No. 2e-5:
58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Score
                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                           5E5868CA919DF969 CRC64;
822.
                                                                                                                                                                               mouse
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RESULT 14
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Best Local Similarity
Matches 153; Conserv
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                                          Q8T068;
Q8T068;
01-JUN-2002
01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8CGU5;
01-MAR-2003
01-MAR-2003
01-MAR-2003
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Ukr. Biokhim. Zh. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/cxC57BLF1; TISSUE=Brain; Skripkina I., Tsyba L., Slavov D., R Skripkina I., Tsyba C., Slavov D., R "Novel splicing forms of human and m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITSN.
Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Hex
                      DAP160 OR CG1099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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                                 D23686p.
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                                                                                                                                                                                                                                         1 HPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
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                                                                                                                                                               RETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPET 860
                                                                                                                                                                                             KGEWVDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLAL
                                                                                                                                                                                                           ----VDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLAL 822
                                                                                                                                                                                                                                                        HPHQEPAKLATQAPWSTTEKGPLTISAQESVKVVYYRALYPFESRSHDEITIQPGDIVM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMPPLTAVAPVPMGSIPVVGMSPPLVSSVPPPAAVPPLANGAPPVIQPLPAFAHPAATWPK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAF-----
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                                                                                                                                                 RETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPET
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158 AA;
                                             (TrEMBLrel.) (TrEMBLrel.)
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation updat isoform 5 (Fragment).
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                                                                                                                                                                                                                                                                                     13.0%;
llarity 96.8%;
Conservative
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17252 MW;
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                                             Last sequence update)
Last annotation updat
                                                                    Created)
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Pred. No. 7.1e-34;
0; Mismatches 0
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0; Mismatches
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 Hexapoda;
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 Pterygota;
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A Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
A Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
A Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
A Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
C --- SIMILARITY: COUTAINS 4 SH3 DOMAINS.
C --- SIMILARITY: COUTAINS 4 SH3 DOMAINS.
R F1yBase; FBgn0023388; Dap160.
R F1yBase; FBgn0023388; Dap160.
R F1yBase; FBgn002388; M3; 4.
R Pfam; PF00018; SH3; 4.
R ProDom; PD000066; SH3; 4.
R ProDom; PD000066; SH3; 4.
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Best Local Similarity
Matches 221; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVQRTSVLELKYNRKNETSVSSAWDT-----GSSSAW-----EETGTTVTDPY-----
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                   ---SEGSG--
                                              FPSNYVQKADVGTASTAAAEPVESLDQETTLNGNAAYTAAPVEAQEQVYQPLPVQEPSEQ
                                                                                   FPSNYVRLKD--
                                                                                                                                                                                                               NHLNFNKSDVITVLEQQDMWWFGEVQGQKGWFPKSYVKLISGPVRKSTSIDTGPTESPAS
                                                                                                                                                                                                                                                                                                                                                 PTPAKPVTDLTSAPAPKLALRETPAPLPVTSSEPSTTPNNWADFSSTWPSSSNEKPETDN
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                                                                                                                                                 LKRVASPAAKPAI PGEEFIAMYTYESSEQGDLTFQQGDVIVVTKKDGDWWTGTVGDKSGV
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                                                                                                                                                                                                                                                                                                                    -APVAAVE---APVDAQVATVADTYN
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SH3 domain protein 1B.
                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional fourth to ENAs.";
Nature 420:563-573(2002).
EMBL; AKO31390; BAC27381.1; -
SEQUENCE 276 AA; 33547 MW; B8BC93085EDC2D7D CRC64;
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Mammalia; Eutheria; Rodentia;
NCBI TaxID=10090;
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=2324603; PubMed=12466851;
The FANTOM Consortium,
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Pred. No. 4e-28;
3; Mismatches
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Sciurognathi; Muridae;
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1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

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17 US-09-764-868-125
18 US-09-764-868-125
19 US-09-864-761-17127
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Sequence 72, Appl
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Sequence 193, Appl
Sequence 195, Appl
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RESULT 1

US-09-884-441-72

Sequence 72, Application US/09884441

Patent No. US20020119158A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darrick

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C7

CURRENT APPLICATION NUMBER: US/09/884,441

CURRENT FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 489

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 72

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222
                                 121 GGTGATCAAGCGAAGCTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA
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  TCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAACGGGGCTCCTCCCGTCATACAGCCT
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Sequence 72, Application US/09907969

Publication No. US20030091580A1

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Algate, Paul A.

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APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Hill, Paul

APPLICANT: Albone, Earl

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C8

CURRENT APPLICATION UNMBER: US/09/907,969

CURRENT APPLICATION UNMBER: US/09/907,969

CURRENT APPLICATION ONMERS: US/09/907,969

CURRENT ELING DATE: 2001-07-17

NUMBER OF SEQ ID NOS: 596

SSETWARE: FastSEQ for Windows Version 4.0

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GENERAL INFORMATION:

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.462C6

CURRENT APPLICATION NUMBER: US/09/827,271

CURRENT FILING DATE: 2001-04-04

NUMBER OF SEQ ID NOS: 461

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 72

LENGTH: 2017

TYPE: DNA

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                                                                           <u> АВТТТВСАТАВАВАСТСВСТТСТТАСССТСАРАВВЕССТТВВАВВСАРАВВЕТВВССТВВСС</u>
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OY 401 NGGCTCCATTCCAGTTGTARGTATCT 444 Db 462 TCTTCTGCTACTTCAGGGACCAGTATTCCTCCCCTAATGATGCCTGCTCCCCTAGTGCCT 521	358 ATTGCTAGCATGCCACCACTCACAGCTGTTGCTCCCTGTGCCAA 1	Qy 301 GTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGGTATAGGAGG 357	QY 241 GCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCT 300	Oy 181 ATATGGGGGCTAGCGGACATGAATAACGATGGAAGGATGGAT	Qy 121 GGTGATCAAGCGAGGAACTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 180	QY 61 GAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTATTACT 120	QY 1 ATGGCTCAGTTTCCCACACCTTTCGGTGGTAGCCTGGATGTCTGGGGCCATAACTGTGGAG 60	Query Match 13:1%; Score 477.4; DB 14; Length 2017; Best Local Similarity 55.5%; Pred. No. 8.6e-127; Matches 1111; Conservative 0; Mismatches 796; Indels 96; Gaps 6;			2 2 2 3 3 S	; APPLICANT: Bangur, Chaitanya S. ; APPLICANT: Retter, Marc W. ; APPLICANT: Fanger, Gary R. ; APPLICANT: Hill Paul	US-10-198-053-72 ; Sequence 72, Application US/10198053 ; Publication No. US20030124140A1 ; GENERAL INFORMATION:		Qy 1912 AGCCTGGAGTTAGAGAAGCAAAA 1934 Db 1995 AGATTAGAGCAAAAAAAAAAAAA 2017	Db 1935 TTAGCCCTTGAACAACTTCATAAAATCAAACGTGACAAATTGAAGGAAATCGAAAGAAA	1852	Qy 1792 GAGATTGATGTTTTCAACCAACCAGCTGAAGGAACTGAGAGAGA	Db 1815 TGCCAAAGACTTAAAGAACAATTAGATGCTCTTGAAAAAGAAACTGCATCTAAGCTCTCA 1874
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Publication No. US20030125246A9
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior application data removed - refer to PALM NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 55
                                                                                                                          Query Match
Best Local Similarity
                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZO7
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (562)
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 568
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                  NAME/KEY: SITE
LOCATION: (556)
                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: n equals a,t,g, NAME/KEY: SITE
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                                      ATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGCCATAACTGTAGAG
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                                                                                                         Score 356; DB 11;
Pred. No. 5.2e-92;
0; Mismatches 64;
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US-09-879-957-193
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                                                                                                                                                                                                          ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/879,957

FILING DATE: 13-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
KAY, Brian K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL,
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                   NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18.872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                      APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                             CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                       TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
       TELEX: 66141 PENNIE
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 2873 bases
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                            CTGGGCAGCTGATTCTGATCCGGAAAAAGAACCCAGGTGGATGGTGGGAAGGAGAACTGC
                                                                                                                                                                                                                                                                                                                                                                  CAAAGGATCAAGAGAGTTTTGGGAGTGCTAGCAAGTCTGGAGCATCAAATAAAAACCTG 1119
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                                                                                                                                                                                                                                                                                                                              AAATTGCCCAGGTTATTGCTTCCTACGCTGCTACTGGTCCCGAACAACTCACCCTGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                    TTAAAGATTCAGAGGGCTCTGGAACTGCTGGGAAAACAGGGAGTTTAGGAAAAAAACCTG 3208
                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTGGTGGACAGGAAGTATTGGAGATAGAAGTGGAATTTTTCCATCAAACTATGTCAAAC 1059
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TATGTCAGGTGATTGCTATGTATGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTCT
                        TGTGCCAGGTGATCGGGATGTACGATTACACCGCCCAGAACGATGACGAACTAGCCTTCA
                                                                                                        AGGCCAGAGGAAAAAAGCGACAGAAAAGGATGGTTTCCTGCCAGTCATGTTAAACTTTTGG
                                                                                                                                                                               AAGCTCGAGGGAAAAAGCGCCAGATAGGGTGGTTTCCAGCAAATTATGTCAAACTTCTAA 3388
                                                                                                                                                                                                                                                                                          AGATTGCTCAGGTAACTTCAGCATATGTTGCTTCTGGTTCTGAACAACTTAGCCTTGCAC
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Pred. No. 9e
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NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 125
LENGTH: 4210
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-764-868-125
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Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Brief and Table 1007-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.1%;
Best Local Similarity 61.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 630;
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                     ACTGGTGGACGGGAACGGTGGGCGAAGTCCGGAGTCTTCCCTTCTAACTATGTGAGGC 3148
                                                                                                                                                                                                                                                                                                                         AGAAGGGTTGGTTCCCCAAGTCTTACGTGAAACTCATTTCAGGGCCCGTAAGGAAATCCA
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                                                                                             CAGCCTATTCAGTT----
                                                                                                                                                                                 CCGCCAAGCCAGCCATTCCCCGGAGAGAGAGTTTATTGCCATGTACACATACGAGAGTTCTG
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AGTGGTGGACAGGAAGTATTGGAGATAGAAGTGGAATTTTTCCATCAAACTATGTCAAAC
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Pred. No. 2.2e-84;
0; Mismatches 361;
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Sequence 31258, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
ITILE OF INVENTION: HOVEL NUCLEIC ACID SEQUENCES OBTITILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION UMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 31258
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US-09-918-995-31258
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                                                                                                                        Query Match
Best Local
                                                                                                          Matches
                                                                                                                                                                                                                                                       LENGTH: 503
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                      FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(503)

OTHER INFORMATION: n = A,T,C or G
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                                                                        823 ACTGCAGAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCA
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                                                                                                                      h 8.9%;
Similarity 81.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCGCCCCTCCTGCCTCCAGAATACATCCCTCCTTCAGAAGAGTTCGCTCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAAGGGACAACTCATTAATGTTATGAACAAAGATGATCCTGATTGGTGGCAAGGAGAGA 1835
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                                                                                                        Conservative
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                                                                                                       Score 322.6; DB 11; Length Pred. No. 2.2e-82; O; Mismatches 84; Indels
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RESULT 9
US-09-879-957-39
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                                                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEVEL...
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
ADDRESSES: Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pateentin Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCGTGAGCGCCAGGAGCAAGAGCGCATAAGACAACTGGAACTGGAGATGCAACTGGGA 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
                                                            LENGTH: 747 bases
                                                                                                                                           TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
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KAY, Brian K.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACTIVITIE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-864-761-17127
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; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-879-957-39
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Best Local S
Matches 418
                                                                                                                                                                                                                                                                 Sequence 17127, Application Patent No. US20020048763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 7.1%;
Local Similarity 63.9%;
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Pred. No. 1.3e-63;
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OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BYA74, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BYA74, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN EXPRESSED IN LUNG, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN HART, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN HART, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN HART, SIGNAL = 2.7

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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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OR APPLICATION NUMBER: PCT/US01/00662
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OR APPLICATION NUMBER: PCT/US01/00661
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00670
OR APPLICATION NUMBER: US 60/234,687
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APPLICATION NUMBER: US .09/608,408
FILING DATE: 2000-06-30
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FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00664
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                                                                                                                                      AAACCAGTGACCGATCTGACATCTGCCCCTGCCCCCAAACTGGCTCTGCGTGAGACCCCT
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87.2%;
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Pred. No. 9.8e-47;
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                                                                                               ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO APO00311.1
OTHER INFORMATION: EXPRESSED IN BI474, SI
OTHER INFORMATION: EXPRESSED IN BONE MARK
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SEQ ID NO 26948
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CURRENT FILING DATE: 2001-05-23
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NUMBER OF SEQ ID NOS: 49117
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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FILING DATE: 2000-10-04
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APPLICATION NUMBER: US 09/608,408
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IN FETAL LIVER, SIGNAL = 32
IN LUNG, SIGNAL = 0.66
IN BRAIN, SIGNAL = 0.69
IN PLACENTA, SIGNAL = 1.1
IN HELA, SIGNAL = 0.92
IN ADULT LIVER, SIGNAL = 0.98
IN ADULT LIVER, SIGNAL = 0.98
IN ADULT LIVER, SIGNAL = 0.98
IN ADULT LIVER, SIGNAL = 0.98
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; OTHER INFORMATION: SWISSPROT HIT: Q15811, EVALUE 2.00e-45; OTHER INFORMATION: EST_HUMAN HIT: AA773263.1, EVALUE 1.00e-112 US-09-864-761-26948
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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Best Local Similarity
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APPLICANT: Rank
APPLICANT: Hanz
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00665
                                                                                             APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                          FILING DATE: 2001-01-30
                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00669
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                        APPLICATION NUMBER: PCT/US01/00661
                                                                    APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                              FILING DATE:
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Hanzel, David K.
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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine; SEQ ID NO 30453
; LENGTH: 297
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Best Local :
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Accomica-Y. CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
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Chen, Wensheng
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NN: EXPRESSED IN HELA, SIGNAL = 1.2

NN: EXPRESSED IN HELA, SIGNAL = 1.2

NN: EXPRESSED IN BT474, SIGNAL = 0.76

NN: EXPRESSED IN HBL100, SIGNAL = 1.3

NN: EXPRESSED IN HBL100, SIGNAL = 1.5

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

NN: EXPRESSED IN BONE MARROW, SIGNAL = 0.95

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Pred. No. 1e-46;
0; Mismatches
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PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
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Matches
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SEQ ID NO 17146
LENGTH: 301
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OTHER INFORMATION: MOTHER INFORMATION
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NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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ORGANISM: Homo sapiens
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00664
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ON: EXPRESSED IN HEART, SIGNAL = 2.2

ON: EXPRESSED IN HELLIO, SIGNAL = 3.2

ON: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3

ON: EXPRESSED IN BRAIN, SIGNAL = 2.6

ON: EXPRESSED IN BLACENTA, SIGNAL = 2.3

ON: EXPRESSED IN BT474, SIGNAL = 2.3

ON: EXPRESSED IN BT474, SIGNAL = 3.4

ON: EXPRESSED IN BLACENTA, SIGNAL = 3.4

ON: EXPRESSED IN HELA, SIGNAL = 3.7

ON: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2

ON: EXPRESSED IN LUNG, SIGNAL = 2.2

ON: SWISSPROT HIT: O35601, EVALUE 3.50e-01

ON: NT HIT: AF114487.1, EVALUE 3.50e-62

ON: EST_HUMAN HIT: BE542917.1, EVALUE 4.00e-62
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82.3%;
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Pred. No. 1.2e-46;
0; Mismatches 49
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                   OTHER INFORMATION: E
OTHER INFORMATION: E
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NUMBER OF SEQ ID NOS: 49117
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                               LENGTH: 263
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/608,408
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FILING DATE: 2001-01-30
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US20020048763A1
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l, David K.
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SSED IN ADULT LIVER, SIGNAL
SSED IN BRAIN, SIGNAL = 4
SED IN BT474, SIGNAL = 3
SED IN BT474, SIGNAL = 3
SED IN HBL100, SIGNAL = 3
DIN LUNG ---
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IN HBL100, SIGNAL = 2.9
IN LUNG, SIGNAL = 3.2
IN HELA, SIGNAL = 3.5
IN FETAL LIVER, SIGNAL = 5.3
IN HEART, SIGNAL = 2.9
IN HEART, SIGNAL = 2.9
HIT: BE542917.1, EVALUE 3.00e-62
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APPLICANT:

Hanzel,

David R.

APPLICANT: Penn, Sharron G.

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; OTHER INFORMATION: SWISSPROT HIT: 035601, EVALUE 2.80e-01; OTHER INFORMATION: NT HIT: AF114487.1, EVALUE 1.00e-122 US-09-864-761-17644
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                                          RESULT 15
US-09-864-761-10314
Sequence 10314, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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Matches 222; Conserv
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
DELICE STITUTE TO THE TOTAL TOTA PRIOR PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03 APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY
FILE REFERENCE: Acomica-X-1 APPLICATION NUMBER: PCT/US01/00665 APPLICATION NUMBER: PCT/US01/00669 FILING DATE: FILING DATE: APPLICATION NUMBER: PCT/US01/00670 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00663 FILING DATE: APPLICATION NUMBER: PCT/US01/00668 2001-01-30 2001-01-30 2001-01-30 2001-01-30 2001-01-30 2001-01-30 PCT/US01/00661 ВУ EXON MICROARRAY PROBES USEFUL FOR

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Search completed: December Job time: 777.554 secs
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Best Local Similarity 81.6%;
Matches 222; Conservative
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SEQ ID NO 10314
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION: EXPRESSED IN BT0474, SIGNAL = 0.87

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 32

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.66

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.69

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.92

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98
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                                                                                                   449 GCCCTCCACGACCCCTAATAACTGGGCCGACT 480
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                        2003, 06:15:46
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 2000000000
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ALIGNMENTS

AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	LOCUS DEFINITION	RESULT 1 AF132478
Sengar, A.S., Wang, W., Bishay, J., Cohen, S. and Egan, S.E. The EH and SH3 domain Ese proteins regulate endocytosis by linking to dynamin and Eps15	Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3723)	Mus musculus (house mouse) Mus musculus	AF132478 AF132478.1 GI:4378884	AF132478 3723 bp mRNA linear ROD 09-MAR-1999 Mus musculus Esel protein mRNA, complete cds.	

Db 61 GATAGGGCCAAGCATGACCAGCTGTTGCTTAGCCTGATACCGGATTACTACTACTACTACACAA 438 Qy 379 GGTGATCAAGCGAGGAACTTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTTTAGCACAA 438 Db 121 GGTGATCAAGCGAGGAACTTTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAA 438 Qy 439 ATATGGGCGTAGCGGACATGAATAACGATGGAATGAACTCAAGTGGAATTTTCCATA 498	Query Match Pack: Score 3721.4; DB 10; Length 3723; Best Local Similarity 100.0%; Pred. No. 0; Matches 3722; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 3722; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Oy 259 ATGGCTCACTTTCCCACACCTTTCCGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAG 318	/product="Bse1 protein" /protein de="An19746.1" /db_xref="G1:43"A019746.1" /db_xref="G1:4378885" /translation="MAQPFPFFGGSLDVWAITVEERAKHDQOFLSLKPIAGFITGDQA /translation="MAQPFPFFGGSLDVWAITVEERAKHDQOFLSLKPIAGFITGDQA RNFFFQGSLDQPULAQIWALADMNIOGRMDQVEFSIAMKLIKLKLQGYQLBSTLPPVM KQQPVAISSAPAFGIGJASMFPLTAVAPVPMGSIPVVGMSPPLVSSVPPAAVPPLAN GAPPVIQPLPAFATHPKSSSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVP QSSRLKYRQLFINSHDKTMSGHLTGPQAAFTILMQSSLPQAQLASIWALSDIQDGKKITA EFILAMHLIDVAMSGQPLPPVLPFYEFDKRESSLPQAKTAILAGQRKEQERLAQLERAEQER KERERQEGEAKRQLELEKQLEKQRELEKRRQALLEGQRKEQERALACERAEQER RRQELLNQRINEQEGTVVLKARKKTLEFELEALIDKKHQLEGKLQDLGERAEQER RRQELLAQRINEQEGTVVLKARKKTLEFELEALIDKKHQLEGKLQDLGERAEQER RRQELLAQQLIREQLDEVERETRSKLQEIDVFNNQLKELERIGRQLEWER RRQECLARQQLGREKGLEKQREDAQREVQERIKGCLGROLKQUQONSLHRDSLLT LKRALEAKELARQQLEREGLDEVERETRSKLQEIDVFNNQLKELERIGRCLKR EBSVRKKEAERBAKERMODGSQMCHEVQCEROKGMLENVQCERQFERKHEEDRLKR EDSVRKKEAERBAKERMODGSQRHEHPHGEPAKLALTFPANWADFSSTWPSSSNE KPETDWMDTMAAQPSLTVPSAGQLRQRSAFTPATATGSSPSVUKGTGWFPANYAEKIP ENEVPTPAKVDHLAFNKSDVITVLEQQDMWWFGEVGGKKWFKYSTSI DTGFTESPASLKRVASSPAKKALEFTPATLEFYSSSEGDLTFQGGCKVEGLQAQAL YPWRAKKDHLAFNKSDVITVLEQQDMWWFGEVGGKKWFFKSVVKLISGPVKKSTSI DTGFTESPASLKRVASSPAKKALTETYABLEVTSSSESSTYTSSSNE KPETDWMDTMAAQPSLTVPSAGGLRQRSAFTPATATGSSPSVVKLISGPVKKSTSI DTGGTTSSPASLKRVASSPAKKALTSTYTSSSEGGTAGKTGSSPSVVKLISGPVKKSTSI DTGGTTSSPASLKRVASSPAKKALTSTYTSSSEGGTAGKTGSSPSVVKLISGPVKKSTSI DTGGTTSSPASLKRVASSPAKKALTSTYTSSSEGGTAGVIASSPATTCPEQLTL APGQLIILIKKAQPGGWFEGELQARGKKGGIGWFFANYVKLLSPOTSKTTPELPKTAV QPAVCQVIGMYDYTAQNDDELAFSKGQIINVLNKEDPDWKKGEVSGQVGLFPSNYVKL BASE COUNT 1065 a 940 C 1026 G 692 t	3.39	
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Mus musculus EselL protein mRNA, complete cds.
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Sengar, A.S., Wang, W., Cohen, S., Bishay, J. and Egan,
Direct Submission
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The EH and SH3 domain Ese proteins
to dynamin and Eps15
EMBO J. 18 (5), 1159-1171 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                    SEDEQQPEKKLPVTFEDKKRENFERGSVLLEKRRQALLEQQRKEGERLAQLERAGER
KERERQEGEAKRQLELEKQLEKQFEEBERKE IERREAAKRELERGRQLEKEKER
KERERQEGEAKRQLELKKQLEKOFEKEREREKE IERREAAKRELERGRQLEWER
NRRQELLUQRNKEQBETVVLKAARKTLEFELBALNDKKHQLEKLQDIRCHLATQRQE
IESTINKSRELR 1AEITHLQQQLQESQQMLGRLIPEKQILSDQLKQVQQNUSHRDSULT
LKRALEKELARQQLREQDEVERETRSKLQEIDVFNNQLKELAEIHSKQQLQKORSL
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59 7	d Q	2179 TTAGAGAAGCAAAAGGAGAGACGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTG 2238	• •
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1 9	Qy Db	1759 CGACTGGCAACCCAGAGGCAAGAAATTGAGAGCACGAACAAGTCTAGAGAGACTAAGAATT 1818	• '
1	Οy	1699 TTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGGTGT 1758 	•
	Ωγ	1639 AACAAGGAGGAGGAGGGCACCGTGGTCCTGAAGGCAAGGAAGAACTCTGGAGTTTGAG 1698 	,
401	. B &	1579 GAPAGGCAGCAACTTGAATGGGAACGGAACCGGAGACAGGAACTCCTGAATCAGAGG 1638 	
ץ ב) B &	1519 CAGCGAGAGGAGGAGGAGGAGGAGGAGGAGGCGCGAGGCCGCAAAACGGGAACTG 1578	• •
281	D &	1459 GAGGCCAAGCGGCAGCTGGAGCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGGCTGGAGCGG 1518 	•
o n - e	D 5	1399 CGGTTGGCTCAGCTGGAGCGCCGAGCAGGAGAGGAAAAGAGCGGGAGCGCCAGGAGCAG 1458 	
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Location/Qualifiers
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1 (bases 1 to 5381)

Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcantara, S., Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Arbones, M.L., Soriano, E., Estivill, X. and Pritchard, M. Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Edit. J. Hum. Genet. 7 (6), 704-712 (1999)
                                                                                                                                                                                                              Submitted (16-DEC-1998) Medical and Molecular Genetics Center, Cancer Research Institute, L'Hospitalet de Llo., Avia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens intersectin AF114488
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EPPKSTALAAVCQVIGMYDYTAQNDDELAFNKGQIINVLNKEDPDWWKGEVNGQVGLF PSNYVKLTTDMDPSQQ" 1192 c 1304 g 1256 t

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Similarity GGGATTTATTACTGGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCC AAGTAACAGAACCATGGCTCAGTTTCCAACACCTTTTGGTGGCAGCCTGGATATCTGGGC ACGTAATAGAACCATGGCTCAGTTTTCCCACACCCTTTCGGTGGTAGCCTGGATGTCTGGGC 305 GGGATGGTGTGCGGGCTGCGGCTCCTGCGTCCCAGCGGCGCGTGAGCGGCACTGA GGGATGGTGTGCGCGCGCTGCGGACTCGGCGTTCCTCGC-GCGGCGTGCGGGGCTGCACTGA 185 CGCGAGGAAGAATCCCGAGCGGGCTCCGGGACG GAGAAGAGTGGAGGCCCAGGGGAGGGAGCGTAGCTTGGTTGCTCCGTAGTACGGCGGCT GAGGAGGAGTGGAGCGCGGGGAGGGCGCGCAGCTTGGTTGCTCCGTAGTACGGCGGCT TGCACTTCCCCCTGTCATGAAACAGCAACCAGTTGCTATTTCTAGCGCACCAGCATTTGG CACACTTCCCCCTGTCATGAAACAGCAACCAGTGGCTATTTTCCAGTGCACCAGCATTTTGG CATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGC TTTGTGTGAGGGGCGGCCGCGCCCCCGGAGATGAGGCGTCGATCAGCAAGGTGA TATGGGAGGTATCGCCAGCATGCCACCGCTTACAGCTGTTGCTCCAGTGCCAATGGGATC TATAGGAGGGATTGCTAGCATGCCACCACTCACAGCTGTTGCTCCTGTGCCAATGGGCTC GGAGTTTTCCATAGCTATGAAACTTATCAAACTGAAGCTACAAGGATATCAGCTACCCTC GGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCTC TGTTTTAGCACAGATATGGGCACTAGCTGACATGAATAATGATGGAAGAATGGATCAAGT CATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGTTCCATAGTTTAAAGCCCAATATC TTTGTCCCTGGGGCGGCAGCGGGACCCGGCGGAGATGAGGCGTCGATTAGCAAGGTAA Conservative 69.4%; 0; Score 3529.4; Pred. No. 0; 0; Mismatches 766; DB 9; Indels Length -GACAGAGAGGCGGGCG 5381; 69; Gaps 485 195 365 245 98 66 495 425 375 315 255 135 675 665 615 605 555 545

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805 GIGGCC	δ 8	1696 GACTTTGGAATTTGAATTAGAAGCTCTAAATGATAAAAAGCATCAACTAGAAGGGAAACT 1755
2745 GCCAGTGACCTCTTCTGAGCCCTCCACAACCCCCAACCACTGGGCAGACTTCAGTTCCAC	D Qy	83 GACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAAAAAGCATCAGCTAGAAGGAAAACT 1
2885 GACCGATCTGACATCTGCCCCTGCCCCCAAACTGGCTCTGGTGAGACCCCTGCTCCTTT	מס	1623 ACTCCTGAATCAGAGGAACAAGGAGCAGGAGGGCACCGTGGTCCTGAAGGCAAGGAGGAA 1682
625 CCCTGC	Db 49	1563 CGCAAAACGGGAACTGGAAAGGCAGCGACAACTTGAATGGGAACGGGAACCGGAGACAGGA 1622
565 AAGCCA 596 AAGCCA	Db Q	1503 GCGGGAGCTGGAGCGGCAGGAGGAGGAGGAGAGGAGAGG
520 CGATGA	y dd d	1443 GAAGCGCCAGGAGCAGGAGCCAAGCGGCAGCTGGAGACTGGAGAAGCAGCTGGAGAAGCA 1502
60 ACAGGA	Db Qy	1383 GCGCAAAGAGCAGGAGCTGGCTCAGCTGGAGCGCGCCGAGCAGGAGAGAGA
400 TAAGCT	Db Q	1323 GAACTTCGAGCGAGGCAGTGTGGAGCTGGAGGAGAGCGCCCAAGCGCTCTTGGAGCAGCA 1382
2340 AGCCAAGCCGGAAATGCAAGACAAGCAGAGTCGGCTTTTCCATCCGCATCAGGAGCCAGC	Db Qy	1266 GGATGAGCAGCAGCCAGAGAAGAACTGCCTGTGACATTTGAAGATAAGAAGCGGGA 1322
1280 CCACGA 1296 CCACGA	Q dd	1206 GATGTCCGTCATAAGCTCTTCTTCTGTGGATCAGAGGCCTGCCT
3 GGACAP 6 GGACAP	Db Qy	1146 GCCCGTCCTGCCAGAATACATCCCTTCCTTCAGAAGAGTTCGCTCCGGCAGTGG 1205
3 GAGGAF 6 ACGAAF	Qy Qy	1086 AGAAGAATTTATCCTAGCTATGCACCTAATTGATGTTGCCATGTCTGGTCAGCCACTGCC 1145
ACAGCI GCAACI	dg dg	1026 GGCTCAGCTGGCTTCAATATGGAATCTTTCTGACATTGATCAAGATGGAAAAACTCACTGC 1085
2043 GCTGCAGGAGATTGATGTTTTCAACAACCAGCTGAAGGAACTGAGAGAGA	dg VQ	966 GAGTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCA 1025
1983 GCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGACGAGGTGGAGAGAGA	B &	906 TGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGCCACGACAAAACTAT 965
	B &	846 TAAGTTACAGAAGGCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGC 905
1863 AATGCTTGGAAGACTTATTCCAGAGAAACAGATACTCAGTGACCAGTTAAAACAAGTCCA 1922 	B &	786 AGCCACATGGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACAC 845
1803 TAGAGAGCTAAGAATTGCTGAAATCACCCACTTACAGCAGCAGTTGCAGGAATCTCAGCA	D Qy	726 TCCCCTGGCTAACGGGGCTCCTCCCGTCATACAGCCTCTGCCTGC
56]	Qy Db	666 CATTCCAGTTGTTGGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCC 725

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Query Match 69.2%; Score 3517.2; DB 10; Length 4025;	/COGON_SEAT=1 //product="BH- and SH3-domain containing protein EHSH1" //protein_id="AAD30271.1" //db_xref="Gi-"aAD30271.1" //db_x	/organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="caxon:10116" CDS	Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, T. 75235, USA FEATURES Location/Qualifiers source 14025	J. Biol. Chem. 274 (26), 18446-18454 (1999) 99303609 10373452 2 (bases 1 to 4025) 2 (kamoto, M., Schoch, S. and Sudhof, T.C. Direct Submission Submission	I (bases 1 to 4025) I (bases 1 to 4025) Okamoto,M., Schoch,S. and Sudhof,T.C. EHSH1/intersectin, a protein that cor binds to dynamin and SNAP-25. A prote exocytosis and endocytosis?		RESULT 4 AF127798 LOCUS AF127798	Qy 5002 TGTGTGTTAACTTGTGCTGTAGCTGAAGCCGTGTGTCCTTAGATATTAGTTGGAAGT	
Oy 1239 GAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAGCAGCAGAGAAACTGCCTGT 1298	Oy 819 ATCTGGTCCAGGTTCAATTAACACTAACTTACAGAGCCACAATCATTCCAGGTCCAGGTCCAGGTCCAGGTCCAATTACAGACACTAACTA		TX Qy 699	Db 361 GGCCATCTCTAGTGCACCAGCGTTTGGTATAGGAGGATGGCTGGAATGCCACCACTGAC Qy 639 AGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTTGGAATGTCTCCACCCTTAGT	and Db 301 Qy 579	Qy 399 TITTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAAATATGGGCGGTAGCGGACAT 458	339 GCAGTICCTTAGCCTGAAGCCGATAGCGGGGATTTATTACTGGTGATCAAGCGAGGAACTT	279 TTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAAGGGCCAAGCATGACCA	Best Local Similarity 93.4%; Pred. No. 0; Matches 3734; Conservative 0; Mismatches 243; Indels 21; Gaps 5; Qy 219 GAGATGAGGGGTCGATCAGCAAGGTAACGAACCATGGCTCAGTTTCCACACC 278

0 0 0	259 GCAGCCACGCCCCGGAAACCCCACGAGGAGACAGACTGAAGAGGGAAGACAGTGTCAG	9 CGCTCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTGGAGCATGTGCAGCAGGAGGA 22 	139 GCGACTGAAGCAGAAAAGAGCAGGAGAGGAAGAGCCTGGAGTTAGAGAAGCAAAAGGAAGA 21 	GGAACTGAGAGAGATACATAGCAAACAGCAACTCCAGAAGCAGAGGTCCCTGGAGGCAGC 21	9 GGTGGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTGAA 2 	CAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCAGGAGCAGCTGGACGA 2	681 C	39 GCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTTATTCCAGAGAAACAGATACT 18 		9	1659 CGTGGTCCTGAAGGCAAGGAAGACTCTGGAGTTTGAGTTAGAAGCTCTGAATGACAA 1718 	1599 ATGGGAACGGAACCGGAGACAGGAACTCCTGAATCAGAGGAACAAGGAGGAGGAGGAGGACAC 1658	39 21	1479 GCTGGAGAAGCAGCTGGAGAGCAGCGGAGCTGGAGCGAGAGGAGGAGGAGGAG 1538	1419 CGCCGAGCAGGAGAAGAGAGCGGGAGCGCCAGGAGCAGGAGCCGAAGCGGCAGCTGGA 1478	1359 CCGCCAAGCGCTCTTGGAGCAGCAGCGCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCG 1418	1021 GCGGCTGCCCGAGGAGCCATCGTCAGAGGATGAGCAGCAGGTGGAAAAGAAGCTGCCTGT 1080 1299 GACATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGAGCAGTGTGGAGCTGGAGAAGCG 1358
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Direct Submission
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3564 TGGATGGTGGGAAGGAGAACTGCAAGCTCGAGGGAAAAAGCGCCCAGATAGGGTGGTTTCC 3623	3504 TCCCGAACAACTCACCCTGGCTCCTGGGCAGCTGATTCTGATCCGGAAAAAGAACCCAGG 3563	3444 AGGGAGTTTAGGAAAAAAACCTGAAATTGCCCAGGTTATTGCTTCCTACGCTGCTACTGG 3503	3384 CTTCCCTTCTÄACTATGTGAGGCTTAAAGATTCAGAGGGCTCTGGAACTGCTGGGAAAAC 3443		3264 CATGTACACATACGAGAGTTCTGAGCAAGGAGATTTAACCTTTCAGCAAGGGGATGTGAT 3323	3204 TCTAAAGAGAGTGGCTTCCCCGGCCGCCAAGCCAGCCATTCCCGGAGAAGAGTTTATTGC 3263	3144 TTCAGGGCCCGTAAGGAAATCCACAAGCATCGATACTGGCCCTACTGAAAGTCCTGCTAG 3203	3084 GTGGTTTGGAGAAGTTCAAGGTCAGAAGGGTTGGTTCCCCAAGTCTTACGTGAAACTCAT 3143	3024 CAACCACTTAAATTTTTAACAAAAGTGACGTTCATCACCGTTCTGGAACAGCAAGACATGTG 3083	2964 GGGTGAAAAGGTGGAAGGGCTACAAGCCGCAAGCCCTGTATCCCTGGAGAGCCAAAAAAAA	2904 GAGATCAGCCTTTACCCCACGCCACAGCCACTGGCTCCTCCCCATCTCCCGTCCTGGGCCA 2963	2844 CTGGGATACGTGGGCGGCTCAGCCTTCTCTGACCGTACTGGTCGCCAGTTACGGCA 2903	2784 CTGGGCAGACTTCAGTTCCACGTGGCCCAGCAGCAGCTCAAACGAAAGCAGAAACGGACAA 2843	2724 GCGTGAGACCCCTGCTCTTTGCCAGTGACCTCTTCTGAGGCCCTCCACAACCCCCAACAA 2783	2664 TCCCACTCCAGCCAAACCAGTGACCGATCTGACCATCTGCCCCTGCCCCCAAACTGGCTCT 2723	2604 GAAAGGGAAGACGGGATGGTTCCCTGCAAACTATGCAGAAAAGATTCCAGAAAATGAGGT 2663 	2556	2353 CCCTTTGAATCCAGAAGCCATGATGAAATCACTATCCAGCCAG
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Okamoto,M., Schoch,S. and Sudhof,T.C.
EHSHI/intersectin, a protein that contains EH and Shinds to dynamin and SNAP-25. A protein connection exocytosis and endocytosis?
J. Biol. Chem. 274 (26), 18446-18454 (1999)
                                                                                                                                                                                                                              Okamoto,M., Schoch,S. and Sudhof,T.C.
Direct Submission
Submitted (02-MAR-1999) Center for Basic Neuroscience and HHMI,
Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX
                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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EEFILAMHLIDVAMSGQPLPPVLPEYIPPSYRRVRSGSGMSVISSSADQRLPEEPS
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Matches 3535; Similarity GAGATGAGGCGTCGATCAGCAAGGTGAACGTAATAGAACCATGGCTCAGTTTCCCACACC GAATAAGGACGGAAGGATCAGGTGGAGTTTTCCATAGCCATGAAGCTCATCAAACT GCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACTGGTGATCAAGCGAGGAACTT GTTATTCAACAGCCACGACAAAACTATGAGTGGACACTTAACAGGTCCCCAGGCAAGAAC CAGCGCCCCCCAGCAGCAGAATGGGCTGTGCCTCAGTCATGAAGGCTGAAATACAGGCA ATCTTCTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAACGGGGCTCCTCCCGTCATACA GAAGCTACAAGGATATCAGCTCCCCCTCCACACTTCCCCCTGTCATGAAACAGCAACCAGT GAATAACGATGGAAGGATGGATCAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACT TTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAAATATGGGCGCTAGCGGACAT TTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAAGGGCCAAGCATGACCA GAGATGAGGCGTCGATTAGCAAGGTAAAGGTAACAGAACCATGGCTCAGTTTCCGACACC CAGCGCCCCTGCAGCGGCAGAATGGGCTGTGCCTCAGTCGTCAAGACTGAAATACAGGCA ATCTGGTCCAGGGTCACAATTAAACACTAAACTACAGAAGGCACAATCATTTGATGTAGC ATCTTCTGTCCCTCAAGCAGCAGTGCCTCCCCTGGCTAACGGGGCCCCTCCTGTCATACA AGCTGTTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTTGGAATGTCTCCACCCTTAGT GGCCATCTCTAGTGCACCAGCGTTTGGTATAGGAGGGATGGCTGGAATGCCACCACTGAC TTTTGGTGGGAGCCTGGACATCTGGGCCATAACCGTGGAGGAAAGAGCCAAGCATGACCA ATCTGGTCCAGGGTCACAATTAAACACTAAGTTACAGAAGGCACAATCATTCGATGTCGC AGCTGTTGCTCCCGTGCCAATGGGCTCCATCCCAGTTGTTGGAATGTCTCCGCCCTTAGT 1088 Conservative gu 972 61.0%; 88.4%; o 1058 0; Score 3103.6; Pred. No. 0; Mismatches ω 694 DВ 229; 10; Indels 234; Length Gaps 338 638 578 120 720 660 600 818 540 758 480 869 420 360 300 518 240 180 60 998 9

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3024 CAACCACTTAAATTTTAACAAAAGTGACGTCATCACCGTTCTGGAACAGCAAGACATGTG	dg VQ	959 CAAAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGACGA	3 8 1
2964 GGGTGAAAAGGTGGAAGGGCTACAAGCGCAAGCCCTGTATCCCTGGAGAGCCAAAAAAGA 	Qy dd	899 CAGTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCATAGAGACTCGCTTCTTACCCT 19	음 성
2904 GAGATĈAGCCTTTACCCCAGCCACAGCCACTGGCTCCTCCCCATCTCCCGTCCTGGGCCA	d VQ	839 GCAGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTTATTCCAGAGAAACAGATACT 18 	음 성
2844 CTGGGATACGTGGGCGCTCAGCCTTCTCTGACCGTACTGATGCTGGCCAGTTACGGCA	β δ	1779 AGAAATTGAGAGCACGAACAAGTCTAGAGAGCTAAGAATTGCTGAAATCACCCACTTACA 1838 	B 8
784 578	Qq dq	1719 AAAGCATCAGCTAGAAGGAAAACTTCAGGATATCAGGTGTCGACTGGCAACCCAGAGGCA 1778	B 8
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458	B &	1599 ATGGGAACCGGAACCGGAGACACGGAACTCCTGAATCAGAGGAACAAGGAGCAGGAGGGCAC 1658	용 <i>청</i>
398	, B &	1539 GAAGGAGATCGAGAGGCGCGAGGCCCGCAAAACGGGAACTGGAAAAGGCAGCGACAACTTGA 1598 	음 성
338	}	1479 GCTGGAGAAGCAGCTGGAGAAGCAGCGGGAGCTGGAGCGGCAGCGAGAGGGAGG	B 8
499 CCCCTTTGAATC	b Q	1419 CGCCGAGCAGGAGAGAGAAGAGAGCGGGAGCAGGAGGAGG	음 성
2439 AGGCCGCTTACCATTTCTGCACAGGAGAGTGTAAAAGTGGTATATTACCGAGCGCTGTA	Db .Q	1359 CCGCCAAGCGCTCTTGGAGCAGCAGCGCAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCG 1418	å å
379 161	Db Q	1299 GACATTTGAAGATAAGAAGCGGGAGAACTTCGAGCGAGGCAGTGTGGAGCTGGAGAAGCG 1358	문 왕
101	B &	1239 GAGGCTGCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAGCAGAGAAGAACTGCCTGT 1298	8 성
041) B &	1179 CTTCAGAAGAGTTCGCTCCGGCAGTGGGATGTCCGTCATAAGCTCTTCTTCTGTGGATCA 1238 	유 성
981	, B &	1119 TGTTGCCATGTCTGGTCAGCCACTGCCGCCCGTCCTGCCTCCAGAATACATCCCTCCTTC 1178	B 8
921) B &	1059 CATTGATCAAGATGGAAAACTCACTGCAGAAGAATTTATCCTAGCTATGCACCTAATTGA 1118	B 8
079	B &	999 TATTCTCATGCAATCAAGTTTACCCCAGGCTCAGCTGGCTTCAATATGGAATCTTTCTGA 1058	용 <i>성</i>
		721 GTTATTCAACAGTCACGACAAGACCATGAGTGGACACTTAACAGGTCCCCAGGCAAGAAC 780	뭣

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                          GGGGCTTTCCTAGTCACTCAGACTGACCGGCCCCGCCT
                                                                                                                      AGTCACTGCGTGCAGAGGCAGAAGCAAATTGCAGAACTGCACAGGGGTGGTGGGTCCTTTT
                                                                                                                                                                                     GAACTCACTGCAGAGCAGTTTACCTCATTTGACCTTAGTTGCATGTGATCGAAATGTCTG
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- GTGCTTTCCTAGTCACTCAGACTGACGGCCCCGCCTT
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1 (bases 1 to 6439)

Pucharcos, C., Fuentes, J.J., Casas, C., de la Luna, S., Alcantara, S., Albertos, C., Soriano, E., Estivill, X. and Pritchard, M. Alu-splice cloning of human Intersectin (ITSN), a putative multivalent binding protein expressed in proliferating and differentiating neurons and overexpressed in Down syndrome Eur. J. Hum. Genet. 7 (6), 704-712 (1999)
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Submitted (16-DEC-1998) Medical and Molecular Genetics Center,
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Pucharcos, C., Fuentes, J.
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                                       Research Institute, L'Hospitalet de ilo., Avia.
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Qy 966 GAGTGGACACTTAACAGGTCCCCAGGCAAGAACTATTCTCATGCAATCAAGTTTACCCCA 1025	QY 906 TGTGCCTCAGTCATCAAGGCTGAAATACAGGCAGTTATTCAACAGGCACGACAAAACTAT 965	OY 846 TAAGTTACAGAAGGCACAATCATTCGATGTCGCCAGCGCCCCTCCAGCAGCAGAATGGGC 905	Qy 786 AGCCACATGGCCAAAGAGTTCTTCCTTCAGCAGATCTGGTCCAGGGTCACAATTAAACAC 845	Qy 726 TCCCCTGGCTAACGGGGCTCCTCCCGTCATACAGCCTCTGCCTGC	OY 666 CATTCCAGTTGTTGGAATGTCTCCACCCTTAGTATCTTCTGTCCCTCCAGCAGCAGTGCC 725	QY 606 TATAGGAGGATTGCTAGCATGCCACTCACACTCATTGCTCTCTGTGCCAATGGGCTC 665	OY 546 CACACTTCCCCCTGTCATGAAACAGCAACCAGTGGCTATTTCCAGTGCACCAGCATTTGG 605	Qy 486 GGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGCTACAAGGATATCAGCTCCCCCTC 545	Qy 426 TGTCTTAGCACAAATATGGGCGCTAGCGGACATGAATAACGATGGAAGGATGGAT	Qy 366 GGGATTTATTACTGGTGATCAAGCGAGGAACTTTTTTTTCCAATCTGGGTTACCTCAGCC 425	OY 306 CATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGTTCCTTAGCCTGAAGCCGATAGC 365	OY 246 ACGTAATAGAACCATGGCTCAGTTTCCCACACCTTTCGGTAGCCTGGATGTCTCGGC 305	QY 186 TTTGTGTGAGGGGCGCCGCCGCACCCGGCAGATGAGGGTCGATCAGCAAGGTGA 245	Qy 127 GGGATGGTGTGCGCGGTTGCGGACTTCGCTCGC-GCGGCTGCGGGTGCACTGA 185	Qy 67 CGCAAGGGAGCATCCCGAGCGGGCTCCGGGACGGCCGGGAGGCAGGC	Qy 7 GAGGAGGAGTGGAGCGCGCGGAGCGCGCAGCTTGGTTGCTCCGTAGTACGGCGGCT 66	Query Match 58.5%; Score 2975; DB 9; Length 6439; Best Local Similarity 86.0%; Pred. No. 0; Matches 3367; Conservative 0; Mismatches 515; Indels 33; Gaps 5;
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REFERENCE JOURNAL MEDLINE PUBMED TITLE AUTHORS

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2 (bases 1 to 7247)
Guipponi,M., Scott,H.S.,
Antonarakis,S.E.

Chen, H.,

Schebesta, A.,

Rossier, C.

and

VERSION KEYWORDS SOURCE ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 7247) Guipponi, M., Scott, H.S., Chen, H., Schebesta, A., Rossier, C. and Antonarakis, S.E. Two isoforms of a human intersectin brain-specific alternative splicing Genomics 53 (3), 369-376 (1998) 99017974 Homo sapiens intersectin long AF064244 AF064244.1 GI:3859854 Homo sapiens (human) AF064244 7247 bp 'ng form r mRNA, (ITSN) protein are in a stop codon linear PR complete cds. PRI produced 21-NOV-1998 γď

DB 133 TGGGAGCCTGGATATCTGGGACTATACTGTAAGGGAAGAAGCATGATCAACGGGAGAACCATGATCAACGAGGATTATTTTTTTT	CDS //dev_stagg="tetus" //docdn.geture_stagg="tetus" //codn.geture_stagg="tetus" stagg="tetuse_stag
225 73 285	SOURCE 174/ / cyganism="Homo sapiens" / db xref="taxon:9606" / chromosome="21" / chromosome="21" / tissue_type="brain" / dev_stage="fetus"
QY 165 GCGGCGTGCGGGCTGCACTGATTTGTGTGAGGGGCGGCGCGCGC	TITLE Direct Submission JOURNAL Submitted (05-MAY-1998) Genetics and Microbiology, CMU, 1 rue Michel-Servet, Geneva 4 CH-1211, Switzerland FEATURES Location/Qualifiers SOURCE 1 7247

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319 GAAGAAGGAGGCGGAAGAGAGACCCGGAAATGCAAGACAAGCAGAGTCGGCTTTT	2259 GCAGCCACGCCGGAAAACCCCCACGAGGAGGAGAGACTGAAGAGGGAAGAGAGAG	TCAGAGACGAGTTCAGGAAAGGGACAAGCAATGGCTGGAGCATGTGCAGCAGGAGGA	ACTGAAGCAGAAAGAGCAGGAGGAGGAAGAGGAAGAGGAAGACGC 2	ACTGAGAGAGATACATAGCAAACAGGAACTCCAGAAGCAGAGGTCCCTGGAGGCAGCGCG	GARGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTGAAGGA	AGAGCCTTGGAAGCAAAGGAGCTGGCCGGCAGCACCTACGAGAGCAGCTGGACGAGGT 	TGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCATAGAGACTCGCTTCTTACCCTCAA	1842 GCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTTATTCCAGAGAAAACAGATACTCAG 1901	AATTGAGAGCACGAACAAGTCTAGAGAGCTAAGAATTGCTGAAATCACCCACTTACAGCA	1722 GCATCAGCTAGAAGGAAAACTTCAGGATATCAGGTGTCGACTGGCAACCCAGAGGCAAGA 1781		1602 GGAACGGAACCGGAGACACGAACTCCTGAATCAGAGGAACAAGGAGCAGGAGGAGCACGGT 1661 	1542 GGAGATCGAGAGGCGGAGGCCGCAAAACGGGAACTGGAAAGGCAGCGACACTTGAATG 1601 	1482 GGAGAAGCAGCTGGAGAAGCAGCGGGAAGCTGGAGCGGCAGCGAGAGGAGGAGGAGGAGGAGGAAGAAGAA	1422 CGAGCAGGAGAAGAACGGGAGCCCAGGAGCAGGAGCCAAGCGGAGCTTGGAGCT 1481	1362 CCAAGCGCTCTTGGAGCAGCAGCGCGAAAGAGCAGGAGCGGTTGGCTCAGCTGGAGCGGG 1421	1302 ATTTGAAGATAAGAAGCCGGAGAACTTCGAGCGAGGCAGTGTGGAGCTGGAGAAGCGCCC 1361	1245 GCCTGAGGAGCCGTCGTCAGAGGATGAGCAGCAGCCAGAGAAGAACTGCCTGTGAC 1301
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99030416
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Intersectin, a novel adaptor protein with two Eps15 homol five Src homology 3 domains
J. Bjol. Chem. 273 (47), 31401-31407 (1998)
                                                                                                                                                                                                                                       Submitted (30-OCT-1997) Pharmacology, University Ave, Madison, WI 53706-1532,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Xenopus laevis intersectin mRNA,
                                                                                                                                                                                                                       University Ave, Madison, WI 
Location/Qualifiers
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Hoffman, N.G., Hardison, N.L., Yamabhai, M. and Kay, B.K.
                                                                                                                                                                                                                                                                                   Direct Submission
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/note="EH domain and SH3 domain containing protein;
similar to intersectin binding proteins Ibp1, encoded GenBank Accession Number AF057285, and Ibp2, encoded b GenBank Accession Number AF057286, and mouse
Rab/Rip,encoded by GenBank Accession Number AF057287"
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/translation="MAQFGTFFGGNLDIWAITVEERAKHDQQFHGLKPTAGYITGDQA
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Query Match
Best Local Similarity
Matches 2713; Conserv CCTTTCGGTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAGGGCCAAGCATGAC CTARARCTACARGGTTACCCGTTGCCCTCTATTCTCCCTTCCAATATGTTGAAGCAACCG ATGAACAATGATGGGAGGATGGACCAACTGGAGTTCTCCATAGCTATGAAATTAATCAAG ATGAATAACGATGGAAGGATGGATCAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAA TTTTTTTTCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAAATATGGGGCGCTAGCGGAC '456 CAGCAGTTCCATGGGCTCAAGCCCAACAGCTGGATATATCACAGGTGACCAAGCTAGGAAT CAGCAGTTCCTTAGCCTGAAGCCGATAGCGGGATTTATTACTGGTGATCAAGCGAGGAAC CCGTTTGGGGGTÄATTTGGÄCATCTGGGCCÄTÄÄCGGTGGAGGAACGAGCTAAACATGAC CCGCTATGAGGCACCTACTAGCAAGCTAATAGTGATACAACCATGGCTCAGTTTGGAACT CGGAGATGAGGCGTCGATCAGCAAGGTGAACGTAATAGAACCATGGCTCAGTTTCCCACA 276 CTGAAGCTACAAGGATATCAGCTCCCCTCCACACTTCCCCCTGTCATGAAACAGCAACCA TTTTTCCTTCAGTCCGGCCTCCCCCAGCCTGTGCTGGCACAGATATGGGCCCCTGGCTGAC Conservative 40.3%; 4. Score 2047.2; Pred. No. 0; 4; Mismatches 932; DВ 5 Indels Length 4103; 39; Gaps 576 510 516 330 396 450 390 270 336 210

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TGGTGGAAAGGAGAACTGAATGGCCATGTTGGTCTGTTTCCCTCCAACTACGTGAAACTG
                                   TGGTGGAAAGGAGAAGTCAGTGGGCAAGTTGGGCTCTTCCCATCCAATTATGTAAAGCTG
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Best Local Similarity
Matches 1832; Conserv
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2599 22-JAN-2002;

HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2599
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PF 1705H10 OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI TURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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1 (Dases 1 to 2131)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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JP 2002017375-A/2599.
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TCCTTAGCCTGAAGCCGATAGCGGGATTTATTACTGGTGATCAAGCGAGGAACTTTTTTT
                                                                       GTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGT
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                                                 GTGGCAGCCTGGATATCTGGGCCATAACTGTAGAGGAAAGAGCGAAGCATGATCAGCAGT
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mer for synthesizing full-length cDNA and use thereof FH R
Location/Qualifiers
CDS (205) (2130)
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07-JUL-2000 JP 2000253172
TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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              CCGAGCAGGAGAGGAGGAGCGGGGGGGGGGCCAGGGAGGCCAGCGAGCTGGAGC
                                                               GCCAAGCGCTCTTGGAGCAGCAGCGCAAAGAGCGGAGGAGCGGTTGGCTCAGCTGGAGCGCG
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REFERENCE AUTHORS

Unpublished
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Isogai, T. and Otsuki, T.

NEDO human cDNA sequencing

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM Homo sapiens to Homo sapien Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K. AK074554.1 GI:22760070 oligo capping; fis (full insert Homo sapiens (human) Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Homo sapiens sapiens 2131 bp cDNA FLJ90073 fis, cl ens intersectin short Craniata; Vertebrata; Catarrhini; Hominidae; mRNA linear clone HEMBA1004110, rt form mRNA. sequence) Euteleostomi; PRI 03-SEP-2002 highly similar

Qy	DЬ	Ş	당 왕	Db Qy	Db Q	₽ <i>Q</i>	B 8	B 8	B 8	dg dg	D QY	D Q	Query M Best Lo Matches	BASE COUNT		FEATURES source		COMMENT	TITLE JOURNAL
704 CTGTCCCTCCAGCAGCAGTGCCTCCCCTGGCTAACGGGGCTCCTCCCGTCATACAGCCTC 763		TTGCTCCTGTGCCAATGGGCTCCATTCCAGTTGTTGGAATGTCTCCACCCTTAGTATCTT	584 TTTCCAGTGCACCAGCATTTGGTATAGGAGGGATTGCTAGCATGCCACCACCACCTCACAGCTG 643	524 TACAAGGATATCAGCTCCCCCTCCACACTTCCCCCTGTCATGAAACAGCAACCAGTGGCTA 583	464 ACGATGGAAGGATGGATCAAGTGGAATTTTCCATAGCCATGAAGCTTATCAAACTGAAGC 523 	404 TCCAATCTGGGTTACCTCAGCCTGTCTTAGCACAAATATGGGCGCTAGCGGACATGAATA 463 	344 TCCTTAGCCTGAAGCCGATAGCGGGATTTATTACTGGTGATCAAGCGAGGAACTTTTTTT 403 	284 GTGGTAGCCTGGATGTCTGGGCCATAACTGTGGAGGAAAGGGCCAAGCATGACCAGCAGT 343	224 GAGGCGTCGATCAGCAAGGTGAACGTAATAGAACCATGGCTCAGTTTCCCACACCTTTCG 283	165 -GCGGCGTGCGGCTGCACTGATTTGTGTGAGGGGCGGCGCGCGC	105 GAGGCAGGCAGGCGGGCGGGCGGGATGGTGTGCGCGGACTCCGGCGACTCCTCGC 164	45 GTTGCTCCGTAGTACGGCGGCTCGCAAGGGAGCATCCCGAGCGGGGCTCCGGGACGGCCGG 104	Query Match 31.7%; Score 1610; DB 9; Length 2131; Best Local Similarity 85.5%; Pred. No. 0; Matches 1832; Conservative 0; Mismatches 295; Indels 15; Gaps 3;	694 a	<pre>/db_xref="taxon:9606" /clone="HEMBA1004110" /tissue_type="whole embryo, mainly head" /clone_Tib="HEMBA1"</pre>		Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).	(a-mail:genomicswnri.co.]p, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction:	
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· 9	Query Match Best Local Matches 174	BASE COUNT	FEATURES source				COMMENT	TITLE	REFERENCE	SOURCE ORGANISM	DEFINITION ACCESSION VERSION	RESULT 12 BD158570	B 8	₽ &	₽ Q	р Q	g Qq	g &	Db
7 GAGGAGGAGTGGAGGGGGGGGGGGGGGGGGGGGTTGGTT	Match 27.6%; Score 1404.2; DB 6; Length 2131; Local Similarity 81.0%; Pred. No. 1.2e-311; es 1740; Conservative 0; Mismatches 283; Indels 126; Gaps 4;	/ organisms nome payters /mol_type="genomic DNA" /db_xref="taxon:9606" 691 a 448 c 572 g 420 t	FT	2N5/00 FH K	PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU, PI KEIICHI NAGAI,TETSUJI OTSUKI PC PC PC PC PC PC PC PC PC PC PC PC PC	PD 09-JUL-2002 PD 09-JUL-2000 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SATTO.	Patent: JP 2002191363-A 13413 09-JUL-2002; HELIX RESEARCH INSTITUTE OS Homo sapiens (human) DN TD 2002191363-8/13413	Ishi, S., Sugiyama, T., Wakamatsu, A., Nagal, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof	lae; Ho	or 2002191363-A/13413Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata;	Primer for synthesizing full-length cDNA and use thereof BD158570 BD158570.1 GI:27864328		2141 GACTGAAGCAGAAAGAGCAGGAGAGGAAGAGCCTGGAGTTAG 2182 	2081 AACTGAGAGAGAGATACATAGCAAACAGCAACTCCAGAAGCAGAGGTCCCTGGAGGCAGCGC 2140	2021 TGGAGAGAGAGACCAGGTCAAAGCTGCAGGAGATTGATGTTTTCAACAACCAGCTGAAGG 2080 	1961 AAAGAGCCTTGGAAGCAAAGGAGCTGGCCCGGCAGCAGCTCCGGGAGCAGCTGGACGAGG 2020	1901 GTGACCAGTTAAAACAAGTCCAGCAGAACAGTTTGCATAGAGACTCGCTTGTTACCCTCA 1960 	1841 AGCAGTTGCAGGAATCTCAGCAAATGCTTGGAAGACTTATTCCAGAGAAACAGATACTCA 1900 	1730 AAATTGAGAGCACAAACAAATCTAGAGAGTTGAGAATTGCCGAAATCACCCCATCTACAGC 1789
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3 (chiba 292-0812, Japan CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix
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Masuho, Y. and Kanehori, K.
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Mammalia; Eutheria; Primates;
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TTTGTGTGAGGGGCGCCGCGCCCCGGAGATGAGGCGTCGATCAGCAAGGTGA
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/db_xref="taxon:9606"
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REFERENCE
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TITLE REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS DEFINITION TITLE

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FEATURES JOURNAL Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3241)
Sparks, A.B., Hoffman, N.G., McConnell, S.J., Fowlkes, D.M. and
Kay, B.K.
Cloning of ligand targets: systematic isolation of SH3
domain-containing proteins
Nat. Biotechnol. 14 (6), 741-744 (1996)
98294438 Human SH3 U61166 U61166.1 2 (bases 1 to 3241)
Pirozzi,G., McConnell,S.J., Uves
Direct Submission
Submitted (18-JUN-1996) CYTOGEN
Princeton, NJ 08540, USA 1. .3241 Location/Qualifiers /organism="Homo sapiens"
/mol_type="mRNA" GI:1438932 Uveges, A. and Corp., 307 Fowlkes, D. College Road East

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/protein_id="%H3AC50592.1"
/protein_id="%AC50592.1"
/db xref="d1:1439933"
/db xref="d1:1439933"
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LTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTSKITPTEPPK
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TTGTCCATCCCCCCCCAGGCTTGAAAGTCCTCAAAGAGACCCACTATCCCATATCACTG
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                                                                        CCTCAACAAGGAGGACCCGGACTGGTGGAAAAGGAAAGTCAGTGGGCAAGTTGGGCTCTT
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                                                   CCCATCCAATTATGTGAAGCTGACCACAGACATGGACCCAAGCCAGCAATGAATCATATG
                                                                                                              CCTCAACAAGGAGGACCCTGACTGGTGGAAAGGAAGTCAATGGACAAGTGGGGCTCTT
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                                                                                                 TTTTATTCCAGTTACTTTTCATGGAATGACCTATTTTGAACAAGTAATTTTCTTGACAAG
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                                                                                                                                                                                                     CACTGAGGTCGTTACGATCAACGATATCCACAGTCTCTTTTAGTCTCTGTTACATGAAG
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    - ACAAAAACACCCACTATCAAGGAGTGCCTGTCTGCGGACGATTAAAATGCTGTTCCGGG

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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
JP 2002017375-A/3071
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KU
PI ISHII,
PI YURI KAWAI, AI WAKAWATSU, TOMOYASU SUGIYAMA, )
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Homo sapiens (human)
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1 (bases 1 to 1676)

Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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Primer for
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PI TETSUJI OTSUKI,HISASHI KOGA
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JP 2002017375-A/3071
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07-JUL-2000 JP 2000253172
TOSHIC OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 5.2e-276;
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Search completed: December 4, 2003, 21:34:01 Job time: 12044.2 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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	Sequence 2, Appli	Sequence 34, Appl	Sequence 34, Appl	Sequence 34, Appl	14	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 30, Appl	Patent No. 5210183	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 136, App	Sequence 1, Appli	Sequence 4, Appli	Sequence 4, Appli

US-08-630-915A-38 RESULT 1 Sequence 38, Application US/08630915A Patent No. 6309820 GENERAL INFORMATION: STREET: 115 Avenue of the Americas CITY: New York STATE: New York STATE: New York COUNTRY: USA ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/630,915A FILING DATE: 03-APR-196 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie REGISTRATION NUMBER: 1101-174 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 869-8864/9741 TELEPHONE: (212) 869-8864/9741 APPLICANT: SPARKS, Andrew B. APPLICANT: HOFFWAN, NO. 6309820h APPLICANT: KAY, Brian K. APPLICANT: FOWLKES, Dana M. APPLICANT: MCCONNELL, Stephen J. TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING TITLE OF INVENTION: USING SAME NUMBER OF SEQUENCES: 227 CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie & Edmonds LLP

; TOPOLOGY: unknown ; MOLECULE TYPE: peptide US-08-630-915A-38

TYPE: amino acid STRANDEDNESS:

LENGTH:

462 amino acids

TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

TELEPHONE: (212) /30 TELEPHONE: (212) 869-8864/9741

Query Match 32.8 Best Local Similarity 79.3 Matches 391; Conservative

32.8%; Score 2058.5; DB 4; Length 462; 79.3%; Pred. No. 4.8e-138; Indels 71;

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                                                                                                                                                                                                                                                                                    STREET: 1155 Avenue of the American CITY: New York STATE: New York COUNTRY: USA ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM:
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FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKST NUMBER: 1101
TELECOMMUNICATION INFORMATION:
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APPLICANT:
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APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
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o. 6309820
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Sequence 40, Application US/08630915A Patent No. 6309820 GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
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TOPOLOGY: un
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                                                                                                                     LSFSKGQLINVMNKDDPDWWQGEINGVTGLFPSNYVKMTTDSDPSQQ 509
                                                                                                                                    | LAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSNYVKLTTDMDPSQQ 1213
                                                                                                                                                                                                                  GELQARGKKRQIGWFPANYVKLLSPGTSKITPTELPKTAVQPAVCQVIGMYDYTAQNDDE 1166
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                                                                                                                                                                                                                                                                                                                    KKPTSAAYSVGEEYIALYPYSSVEPGDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSN
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(212) 869-8864/9741
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; Pred. No. 1.9e-90;
85; Mismatches 124;
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                                                                                                                                                                                                                                    Sequence 2, Application US/08095737 Patent No. 5487979
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Best Local Similarity
                                                                                                                         GENERAL INFORMATION:
APPLICANT: Difiore, Pier P
APPLICANT: Fazioli, Francesca
TITLE OF INVENTION: A Substrate for the Epidermal Growth
TITLE OF INVENTION: Factor Receptor Kinase
NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MISCONDING S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      CORRESPONDENCE ADDRESS:
STATE: Cali
COUNTRY: Un
ZIP: 92660
                            ADDRESSEE: Knobbe, Martens, Olson
STREET: 620 Newport Center Drive,
CITY: Newport Beach
STATE: California
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                                                                                                                                                                                                                                                                                                                                              GVTGLEPSNYVKMTTDSDPSQQ 248
                                                                                                                                                                                                                                                                                                                                                                                                                     SSERATPAFHP-----VCQVIAMYDYAANNEDELSFSKGQLINVMNKDDPDWWQGEIN 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQGELQARGKKRQKGWFPASHVKLLGP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSNYVKPKDQESFGSASKSGASNKKPEI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAAASTKIIPGSEVK------REEPEALYAAVNKKPTSAAYSVGEEYIALYPYSSVEP
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                 States of America
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                                                                    & Bear
Sixteenth
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Best Local Similarity
Matches 198; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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REGISTATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 896 amino acids
TYPE: amino acid
TOPOLOGY: linear
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FILING DATE: 19930722
CLASSIFICATION: 530
642
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                                     511 WCSSPHSILVNGATDYCSLSTSSSETANLNEHVEGQSNLESEPIHQESPARSSPELLPSG
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                                                                                                                                                                                                                                                                                                                             EAAKRELEROROLEWERNRROELLINORNKEQEGTVVLKARRKTLEFELEALNDKKHOLEG 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSGMSVISSSSVDQRLPEEPSSEDEQQPEKKLPVTFEDKKRENFERGSVELEKRRQALLE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WAVKPEDKAKYDAIFDSLSPVNGFLSGDKVKPVLLNSKLPVDILGRVWELSDIDHDGMLD
                                                                                                                                                                                                        QLKEVRKKCAEEAQLISSLK-----
                                                                                                                                                                                                                                                                                      NTNLOKLOAOKO-----OVOELLDE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLQKNIIGSSPV-----
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                                                                                                                   LQQETAE-----LEESVESGKAQLEPLQQHLQDSQQEISSMQMKLMEMKDLENHNSQLN
                                                                                                                                                            VQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRS-----KLQEIDVFNNQLK 607
                                                                                                                                                                                                                                           KLQDIRCRLATQRQBIESTNKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILSDQLKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAM-SGQPLPPVLPPEYIPPSFRRVRS 313
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                                                                          ---KQQLQKQRSLEAARLKQKEQERKSLEL----
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181

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203

EKQKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEER-----

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641 510 456 553

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314

Oy 15 WAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQIWALADMNNDGRMD	Query Match 7.8%; Score 486.5; DB 1; Length 896; Best Local Similarity 20.5%; Pred. No. 4.3e-26; Matches 198; Conservative 150; Mismatches 273; Indels 345; Gaps	amino acid Y: linear TYPE: prote 2	98 R (6)	REGISTRATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: NIHO60.001A TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 235-8550	APPLICATION NUMBER: US 08/095,737 FILING DATE: 22-UUL-1993 ATTORNEY/AGENT INFORMATION: NAME: Israelsen. Ned A	APPLICATION NUMBER: US/08/480,145 ; APPLICATION NUMBER: US/08/480,145 ; FILING DATE: 07-JUN-1995 ; CLASSIFICATION: 530 ; PRIOR APPLICATION DATA:	R: IBN	COUNTRY: United States of America ; ZIP: 92660 ; COMPUTER READABLE FORM: MEDITIM TYPE: Florary disk	ADDRESSEE: Knobbe, Martens, Olson & Bear ; STREET: 620 Newport Center Drive, Sixteenth Floor ; CITY: Newport Beach ; STATE: California	(C)	RMATION: Diffiore, Fazioli	RESULT 5 US-08-480-145-2 ; Sequence 2. Application US/08480145	Qy 866 WAAQPS 871 	Qy 831VTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDT : :: :: : : : : : :	Qy 781ELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLP	Qy 739 KVVYYRALYPFESRSHDEITIQPGDIVMVDESQTGEPGWLGG	QY 695AKPEMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTISAQESV	Db 571 VTDENEVTTAVTEKVCSELDNNRHSKEEDPFNVDSSSLTGPVADTNLDFFQS
; Patent No. 5872219 ; GENERAL INFORMATION:	RESULT 6 US-08-477-389-2 29; Sequence 2, Application US/08477389	QY 866 WAAQPS 871	CY 831VTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDT 865	YAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLP	Oy 739 KVVYYRALYPFESRSHDEITIQPGDIVMVDESQTGEPGWLGG 780	Qy 695AKPEMQDKQSRLFHPHQEPAKLATQAPWSTTEKGPLTISAQESV 738	Qy 642 EKQKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKEAEER 694	Qy 608 ELREIHSKQQLQKQRSLEAARLKQKEQERKSLEL 641	Qy 554 VQQNSLHRDSLLTLKRALEAKELARQQLREQLDEVERETRSKLQEIDVFNNQLK 607	Qy 494 KLODIRCRLATOROEIESTIKSRELRIAEITHLQQQLQESQQMLGRLIPEKQILSDQLKQ 553	Qy 434 EAAKRELERQRQLEWERNRRQELLNQRNKEQEGTVVLKARRKTLEFELEALNDKKHQLEG 493 :- :- :- :- :- :- :- :- :- :- :- :- :- :	Qy 374 QQRKEQERLAQLERABQERKERERQEQEAKRQLELEKQLEKQRELERQREEERRKEIERR 433	Qy 314 GSGMSVISSSSVDQRLPEEPSSEDEQQPEKKLPVTFEDKKRENFERGSVELEKRRQALLE 373	865 QY 255 PQAQLASIMNLSDIDQDGKLTAEEFILAMHLIDVAM-SGQPLPPVLPPEYIPPSFRRVRS 313	830 Qy 195 NTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSL 254	780 Qy 135 GSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWPKSSSFSRSGPGSQL 194 : :	738 Qy 75 QVEFSIAMKLIKLKQGYQLPSTLPPVMKQQPVAISSAPAFGIGGIASMPPLTAVAPVPM 134	622 Db 122 WAVKPEDKAKYDAIFDSLSFVNGFLSGDKVKPVLLNSKLFVDILGRVWELSDIDHDGMLD 181

Query Match Best Local Similarity 20.5%; pred. No. 4.36-26; Matches 198; Conservative 150; Mismatches 273; Indels 345; Gaps 29; Qy 15 WAITVEERAKHDQOFLSLKPIAGFITGDQARNFFQSGLDOPVLAQIWALADMNNDGRWD 74	APPLICANT: DiFiore, Pier P APPLICANT: Featoli, Francesca FITIE OF INVENTION: A Substrate for the Epidermal Growth TITLE OF INVENTION: A Substrate for the Epidermal Growth FRIED OF INVENTION: A Substrate for the Epidermal Growth FRIED OF SEQUENCES: 4 CONTECT STREET: 620 Newport Extreme, Olson & Bear ADDRESSEE: Knobbe, Martens, Olson & Bear ADDRESSEE: Knobbe, Martens, Olson & Bear COUNTY: Newport Beach STATE: California COUNTY: POLOS/MS-DOS SOFTWARE: TIBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 COURTENT APPLICATION DATA: APPLICATION NUMBER: US/08/477,389 FILING DATE: 07-JUN-1995 CLASSIFICATION DATA: APPLICATION NUMBER: 08/95,737 FILING DATE: 07-JUN-1995 APPLICATION NUMBER: 08/95,737 FILING DATE: 07-JUN-1995 APPLICATION NUMBER: 08/95,737 FILING DATE: 07-JUN-1995 APPLICATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: N
WESULT 7 (Sequence 4, Application US/08095737 (Sequence 4, Application US/08095737 (Sequence 4, Application US/08095737 (Patent No. 5487979) (GENERAL INFORMATION: (APPLICANT: Distore, Pier P APPLICANT: Pazioli, Francesca (TITLE OF INVENTION: Factor Receptor Kinase (NUMBER OF SEQUENCES: 4 (CORRESPONDENCE ADDRESS: (ADDRESSE: Knobbe, Martens, Olson & Bear (STREET: 620 Newport Center Drive, Sixteenth Floor (CITY: Newport Beach (COUNTRY: United States of America (CONTRY: United States of America (COMPUTER ENDABLE FORM: (MEDIUM TYPE: Floppy disk (COMPUTER IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS (SOFTWARE: Patentin Release #1.0, Version #1.25 (CURRENT APPLICATION DATA: APPLICATION UNMERE: US/08/095,737 FILING DATE: 1930722 (CLASSIFICATION: S30 ATTORNEY/AGBNT INFORMATION: NAME: Israelsen, Ned A REGISTRATION UNMER: US/08/095,737 FILEPAX: (619) 235-0176 INFORMATION FOR SEQ ID NO: 4:	Db 381 NTNLQKLQAQXQQVQELLDE

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 897 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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843 WADFSST-----WPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPATATGSS 895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 KLQDIRCRLATQRQEIESTNKSRELRIAEITHLQQQLQESQQMIGRLIPEKQILSDQLKQ 553
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                                                                740 AFNPTISSSTSSVTIAKPMLEETASKSEDVPPALPPKVGTPTRPCPPP-----PGKRPIN 794
                                                                                                                                                                                                                                                                                                                                                                     654
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                                                                                                          VPTP-----AKPVTDLTSA-----PA--PKLALRETPAPLPVTSSEPSTTPNN 842
                                                                                                                                                    SSNTSVETWICHNDPFAPGGTVVAAASDSATDPFASVFGNESFG-DGFADFSTLSKVNNED 739
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	חסיסי זיקינים בחיים ביים ביים אויני זיקיני אויני דיקינים מיים ביים ביים ביים ביים ביים ביים בי	195 NTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLTGPQARTILMQSSL 254	204SLPPALVPPSKR 215	135 GSIPVVGMSPPLVSSVPPAAVPPLANGAPPVIQPLPAFAHPAATWPKSSSFSRSGPGSQL 194	: : : : : : : : : :	75 QVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPVAISSAPAFGIGGIASMPPLTAVAPVPM 134	122 WAVKSEDKAKYDAIFDSLSFVDGFLSGDKVKFVLLNSKLFVBILGRVWELSDIDHDGKLD 181	AKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQIWALADMNNDGR	7.8%; Score 486; DB 1; Length 897; Local Similarity 21.3%; Pred. No. 4.7e-26; es 205; Conservative 138; Mismatches 298; Indels 322; Gaps 31;	TOPOLOGY: linear MOLECULE TYPE: protein 3-480-145-4		FOR SEQ	2 2	NAME: IRRENTANCE 20 ASS	. 22-JUL-199	2 -	o z	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,145	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25	compatible	READABI) HC	Newport Beach	ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newmort Center Drive. Sixteenth Floor	OF SEQUENCES: 4	S C	ANT: Fazioli, Francesca	AL INFORMATION:	4.		839 ADP 841	896 PSP 898	795 KLDSSDPLKLNDPFQPFPGNDSPKEKDPDMFC

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RESULT 9
US-08-477-389-4
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                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     APPLICANT: DiFiore, Pier P
APPLICANT: Fazioli, France
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                            APPLICANT: Fazioli, Francesca
TITLE OF INVENTION: A Substrate for the Ep
TITLE OF INVENTION: Factor Receptor Kinase
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                       COUNTRY:
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                                                                                                                                                                                E: Knobbe, Martens, Olson & Bear 620 Newport Center Drive, Sixteenth Floor
                                                                                                                           United States of America
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A
REGISTRATION UNMBER: 29,655
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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APPLICATION NUMBER:
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      PETAPSDVTDESEAVTVAGNEKVTPR--FDDDKHSKEEDPFNVESSSLTDAVADTNLDFF
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                                           ER-----DKOWLEHVOOEEOPRPRKPHEEDRLKREDSVRKKEA----EERAKPEMODK 702
                                                                                                                       LREIHSKQQLQKQ-----
                                                                                                                                                              LQQETAQ-----LEESVESGKAQLEPLQQHLQESQQEISSMQMRLEMKDLETDNNQ---
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illarity 21.3%; Pred. No. 4.7e-26;
Conservative 138; Mismatches 298;
                                                                                  SNWSSSPQSVLVNGATDYCSLSTSSSETANFNEHAEGQNNLESEPTHQESSVRSS
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US-08-728-323A-2
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                                                                                                   ; MOLECULE TYPE: US-08-728-323A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application Patent No. 5948676
GENERAL INFORMATION:
                                                                                                                            TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                               Matches
                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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127; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                           6.1%; Score 382; DB 2;
larity 24.6%; Pred. No. 1.6e-18;
Conservative 139; Mismatches 197
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                                                                                                           SSSEDEMEVD----YPVVS-THEQIASSPPGDNTPDDDPQPGPSREYRYVLRTSPPHRP
                                                                                                                                                                 -SAQESVKVVYYRALYPFESRSHDEI-TIQPGDIVMVDESQTGEPGWLGGELKGKTGWFP 790
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; ORGANISM: Kaposi's US-09-298-568-2
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                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
                                                                                                                                                                Matches
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                  LENGTH: 1162
TYPE: PRT
                                      383 AQLERAEQERKERERQEQEAKROLELEKOLEKORELERQREEERRKEIERREAAKRELER 442
                                                                                                                                                              127;
                                                                                                                                                                                   Similarity
QRLPE--EPSSEDEQQ--PEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERL 382
                                                                              Application US/09298568
                                                                                                                                                                Conservative
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                                                                                                                                                                                 6.1%;
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Pred. No. 1.6e-18;
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US-09-410-399-2
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LENGTH: 1162
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                                                                                                                                                                                                                                                                                                                                                                                                      Matches 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Kaposi's sarcoma-associated herpesvirus
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                                                                                                                                                                                                                                                                 QRLPE--EPSSEDEQQ--PEKKLPVTFEDKKRENFERGSVELEKRRQALLEQQRKEQERL
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                                                                                                                                                                                                RSLE--AARLKQKEQERKSLELEKQKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEE-D
                           RSLE--AARLKQKEQERKSLELEKQKEDAQRRVQERDKQWLEHVQQEEQPRPRKPHEE-D
                                                                                                 SLLTLKRALEAKELARQQLREQLDEVERETRSKLQEIDVFNNQLKELREIHSKQQLQKQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%; Score 382; DB 4; 24.6%; Pred. No. 1.6e-18;
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US-08-056-200-94
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                                                                                                                                                                                                            Matches 136;
                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 1898 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/056,200
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth
CITY: Newport Beach
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GY: linear
                           ---RKEIERREAAKRELERQRQLEWERNRRQELLNQRNKEQEGTVVLKARRKTLEFELEA 483
                                                                 EQQLRREQQLRREQQLRREQQLRREQQLRREQQLRREQHEQKHEQERREQ
RLKREQEERROWLKREEETERH---EQERRKQQL-KRDQEEE-----RRERWLKLEEE-
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Park, Sang-Chul
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                                                                                                                                                                                                        Score 381; DB 1;
Pred. No. 3.9e-18;
7; Mismatches 154
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RESULT 14
US-08-800-644-94
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                                                                                                         TELEFAX: (714) 760-950 INFORMATION FOR SEQ ID NO:
                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (714) 760-0404
                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 14-FEB-1997 CLASSIFICATION: 424
                                     TOPOLOGY:
                                                                                                                                                                                             NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
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                                                                     1898 amino acids
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Park, Sang-Chul
Park, Sang-Chul
VENTION: Trichohyalin and Transglutaminase-3
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US-08-475-894-2
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Best Local Similarity
                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, VG

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Yen-Mi
                                              FILING DATE:
CLASSIFICATION: 530
ATTORNEY, AGENT INFORMATION:
NAME: LOUIS MYCTS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yen-Ming
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
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              : (617)227-7400
(617)227-5941
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THE CAIP-LIKE GENE FAMILY
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Pred. No. 3.9e-18
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; SEQUENCE CHARACTERISTICS:

; LENGTH: 5-3 amino acids

TYPE: amino acid

TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-475-894-2
Search completed: December 4, 2003, 15:21:35
Job time: 28 secs
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                                                                                 1109 LQARGKKRQIG-WFPANYVKLLSPGTSKITPTELPKTAVQPAVCQVIGMYDYTAQNDDEL 1167
                                                                                                                                                                                                                                                                                                 1055 GSGTAGKTGSLGKKPEIAQVIASYAATGPEQL-----TLAPGQLILIRKKNPGGWWEGE 1108
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                                                                                                                                                                         307 NDFLPVEKTIGKKLPAT---TATPDSSK---TEMDSRTKSKDYCKVI--FPYEAQNDDEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                    137 LTNKAP-EKP--LHEV--PSGNSLLSSETTLRTNKRGERRRRRCQVAFSYLPQNDDELEL 191
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Result
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Maximum Match 100%
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Perfect score:
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6269
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(cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 38, Appl
Sequence 194, App
Sequence 738, App
Sequence 40, Appl
Sequence 23, Appl
Sequence 133, App
Sequence 132, Appl
Sequence 33620, A
Sequence 34004, A
Sequence 34655, A
Sequence 46565, A
Sequence 4769, Appl
Sequence 128, Appl
Sequence 83, Appl
                                                                                                                                                                                                                                                                                     Description
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US-09-879-957-38
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US-09-298-523B-60	US-09-893-519A-73	US-10-309-851-16	US-10-309-851-14	US-10-082-830-260	US-10-094-749-2682	US-10-309-851-12	US-09-879-957-136	US-10-128-714-8314	US-09-291-417-89	US-10-247-671-157	US-09-771-161A-226	US-09-771-161A-225	US-09-771-161A-224	US-10-321-856-81	US-09-216-393-81	US-10-128-714-3314	US-09-879-957-134	US-09-879-957-135	US-10-144-198-4	US-10-144-198-2	US-10-341-434-95	US-09-764-868-744	US-10-144-194A-108	US-10-144-194A-109	US-09-879-957-133	US-10-144-621-2	US-09-291-417-13	-10	US-10-144-194A-84
60,				260, 1		e 12,	136,	8314	89,	Sequence 157, App	226,		224	æ	Sequence 81, Appl	ø				Sequence 2, Appli			Sequence 108, App	æ			13,	86	Sequence 84, Appl

ALIGNMENTS

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: SPARKS, Andrew B.

KAY, Brian K.

FOMLKES, Dana M.

CONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

LOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

USING SAME

NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

COUNTRY: USA

ZOUNTRY: USA

ZOUNTRY: USA

ZOUNTRY: USA

ZOUNTRY: USA

ZOUNTRY: USA

ZOUNTRY: USA

COUNTRY: USA

ZOUNTRY: USA

ZOUNTRY: USA

ZOUNTRY: USA

COMPUTER: FLORM:

MEDIUM TYPE: FLORM:

MEDIUM TYPE: FLORM:

MEDIUM TYPE: FLORMS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/09/879,957

FILING DATE: 13-Jun-2001

CLASSIFICATION UNMBER: US/09/879,957

FILING DATE: 13-Jun-2001

CLASSIFICATION UNMBER: US/09/879,957

FILING DATE: 03-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: MISTOCK, S. Leelie

REGISTRATION UNMBER: 18,972

REFERENCE/DOCKET NUMBER: 1101-174

TELECOMMUNICATION INFORMATION:

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TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: unknown>
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-879-957-38
                                                                                                                                                                                                                                                                                                                                                          US-09-879-957-194
                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
                                                                                                                                                                                                                                                                                           Sequence 194, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                      APPLICANT: SPARKS, Andrew B.
HOPFMAN, No. US20020034755Alh
KAY, Brian K.
FOULKES, Dana M.
MCCONNELL, Stephen J.
MCCONNELL, Stephen J.
DOMAIN OF INTEREST AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1081
                                                              NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1141 LPKTAVQPAVCQVIGMYDYTAQNDDELAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSN 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1021 VIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYAA 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 32.8%; Score 2058.5; DB 9; Similarity 79.3%; Pred. No. 2.6e-101; 91; Conservative 13; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LISGPVRKSTSIDTGPTESPASLKRVASPAAKPAIPGEEFIAMYTYESSEQGDLTFQQGD 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGPEQLTLAPGQLILIRKKNPGGMWEGELQARGKKRQIGWPPANYVKLLSPGTSKITPTE 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPATATGSSPSPVL 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETPAPLPVTSSEPSTTP 840
                                         ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                            YVKLTTDMDPSQQ 462
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    CITY: New York
STATE: New York
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TELEFAX: (212) 869-8864/9741
                                                                                                                             USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                OF IDENTIFYING
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HOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-879-957-194
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Best Local
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APPLICATION NUMBER: US 08/630,915

FILING DATE: 03-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 110.872

REFERENCE/DOCKET NUMBER: 1101-174

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          local Similarity
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
                                                                                    1107
    1167 LAFSKGQIINVLNKEDPDWWKGEVSGQVGLFPSNYVKLTTDMDPSQQ 1213
                                                                                                                                                                      1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                             350
                                             410
                                                                                                                                                                                                                                                                                                                                                                               181 FSNLTVNTSWQ--KKSAFTRTVSPG-SVSPIHGQGQVVENLKAQALCSWTAKKDNHLNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140
                                                                                                                                                                                                               290 KKPTSAAYSVGEEYIALYPYSSVEPGDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSN 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            751 SRSHDEITIQPGDIVMVDESQTGEPGWLGGELKGKTGWFPANYAEKIP--ENEVPTPAKP 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             635 ERKSLELEKQK----EDAQRRVQERDKQWLEHVQQEEQPRPRKPHEEDRLKREDSVRKKE 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 EEERKAEEKQ------RETASV------LVNYRALYPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                   YVRLKDSEGSGTAGKTGSLGKKPEIAQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWE 1106
                                                                             GELQARGKKRQIGWFPANYVKLLSPGTSKITPTELPKTAVQPAVCQVIGMYDYTAQNDDE 1166
                                                                                                                                                                                                                                 --PAAKPAIPGEEFIAMYTYESSEQGDLTFQQGDVIVVTKKDGDWWTGTVGDKSGVFPSN 1046
                                                                                                                                                                                                                                                                                                                                                                                                                      QPSLIVPSAGQLRQRSAFTPATATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFN 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEERAKPEMODKOSRLEHPHOEPAKLATOAPWSTTEKGPLTISAQESVKVVYYRALYPFE 750
                                                                                                                               YVKPKDQESFGSASKSGASNKKPEIAQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQ 409
                                                                                                                                                                                                                                                                                               KHDIITVLEQQENWWFGEVHGGRGWFPKSYVKIIPGSEVK-----REEPEALYAAVN
                                                                                                                                                                                                                                                                                                                           KSDVITVLEQQDMWWFGEVQGQKGWFFKKSYVKLISGFVRKSTSIDTGFTESFASLKRVAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 509 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                           GELQARGKKRQKGWFPASHVKLLGPSSERATPAFHP----VCQVIAMYDYAANNEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1388.5; DB 9;
Pred. No. 8.3e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version
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US-09-764-868-738
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                                                                   Sequence 40, Application Upatent No. US20020034755A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 738, Application US/09764868 Patent No. US20020168711A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 530
TYPE: PRT
ORGANISM: Homo sapiens
-09-764-868-738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REPERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior application data removed - refer to NUMBER OF SEQ ID NOS: 1510
                                                                                                                                                                                                                                                                                 1129
                                                                                                                                                                                                                                                                                                                                                                                                             1009
                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                 334
                                                                                                                                                                                                                                                                                                                                                                               274
                                                                                                                                                                                                                                                                                                                                                                                                                                                            951 KGWFPKSYVKLISGPVRKSTSIDTGPTESPASLKRVAS--PAAKPAIPGEEFIAMYTYES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            891 ATGSSPSPVLGQGEKVEGLQAQALYPWRAKKDNHLNFNKSDVITVLEQQDMWWFGEVQGQ 950
                                                                                                                                                                                     447
                                                                                                                                                                                                                                                                                                                                                                                                                                             222
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                                                                                                                                                                                                                                                               LSPGTSKITPTELPKTAVQPAVCQVIGMYDYTAQNDDELAFSKGQIINVLNKEDPDWWKG 1188
                                                                                                                                                                                                                                                                                                                                                                                              SEQGDLTFQQGDVIVVTKXDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKK 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTSSEPSTTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPSLTVPSAGQLRQRSAFTPAT
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                                                                                                                                                                                                    EVSGQVGLFPSNYVKLTTDMDPSQQ 1213
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                                                                                                                                                                                                                                                                                                                                                                             VEPGDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSNYVKPKDQESFGSASKSGASNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                           RGWFPKSYVKIIPGSEVK------REEPEALYAAVNKKPTSAAYSVGEEYIALYPYSS
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                                                                                                                                                                                                                                                 LGPSSERATPAFHP-----VCQVIAMYDYAANNEDELSFSKGQLINVMNKDDPDWWQG
                                                                                                  Application US/09879957
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                     SPARKS, Andrew B. HOFFMAN, No. US20020034755A1h KAY, Brian K.
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52.7%; Pred. No. 1e-62;
tive 71; Mismatches 1
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RESULT 5
US-09-764-881-133
; Sequence 133, Application US/09764881
; Publication No. US20030125246A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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Query Match
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les 153; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Pateentin Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Un-2001
CLASSIFICATION: <Unknown>
                                                                                                                           1132
                                                                                                                                                                                                           1072
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                           1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
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                                                                                                                                                                    114
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                     GQVGLFPSNYVKLTTDMDPSQQ 1213
                                                                                                     GTSKITPTELPKTĄVQPAVCQVIGMYDYTĄQNDDELAFSKGQIINVLNKEDPDWWKGEVS 1191
                                                                                                                                                                                                                                                                                                                                  FAAASTKIIPGSEVK-----REEPEALYAAVNKKPTSAAYSVGEEYIALYPYSSVEP
                                                                                SSERATPAPHP-----VCQVIAMYDYAANNEDELSFSKGQLINVMNKDDPDWWQGEIN
                                                                                                                                                                AQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQGELQARGKKRQKGWFPASHVKLLGP
                                                                                                                                                                                              AQVIASYAATGPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSP 1131
                                                                                                                                                                                                                                                  GDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSNYVKPKDQESFGSASKSGASNKKPEI
                                                                                                                                                                                                                                                                          GDLTFQQGDVIVVTKKDGDWWTGTVGDKSGVFPSNYVRLKDSEGSGTAGKTGSLGKKPEI
GVTGLFPSNYVKMTTDSDPSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 248 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-8864/9741
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ZIP: 10036-2711
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STREET: 1155 Avenue of the Amer
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Pred. No. 6.7e-36;
8; Mismatches 54
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US-09-964-899-25
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                                                     Query Match
Best Local S
Matches 197
                                                                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                       Sequence 25, Applica Patent No. US2002017 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior application data removed - refer
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 133
LENGTH: 144
TYPE: PRT
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Best Local :
                                                                                                          TYPE: PRT
ORGANISM: Homo Sapien
-09-964-899-25
                                                                                                                                                                                                                                                        APPLICANT: Cohen, Dalia et al.
TITLE OF INVENTION: Identification of Genes Involved in
TITLE OF INVENTION: Alzheimer's Disease Using Drosophil
FILE REFERENCE: 4-31612 A
CURRENT APPLICATION NUMBER: US/09/964,899
CURRENT FILING DATE: 2001-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZO7 CURRENT APPLICATION NUMBER: US/09/764,881 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/236,893
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/298,309
PRIOR FILING DATE: 2001-06-14
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NAME/KEY: SITE
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LOCATION: (143)
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LOCATION: (141)
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NAME/KEY: SITE
LOCATION: (134)
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  105
                                                     al Similarity
197; Conserv
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  EDKAKYDAI FDSLSPVNGFLSGDKVKPVLLNSKLPVDILGRVWELSDIDHDGMLDRDEFA
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                          EERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQIWALADMNNDGRMDQVEFS 79
                                                                                                                                                                                                                                                                                                                                                                   Application US/09964899
                                                   8.4%; Score 527; DB 10;
larity 21.9%; Pred. No. 5.6e-20;
Conservative 138; Mismatches 283
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Pred. No. 3.1e-23;
6; Mismatches 18
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                                                                              Length 813;
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 132
LENGTH: 224
                                                                                                                                              Sequence 132, Application US/09764881
Publication No. US20030125246A9
                                                                                                                                      GENERAL INFORMATION:
                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ07
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165 VAMPLVYCALEKEPVPMSLPPAL----VPPSKRKTVSISGSVRLIPSSASAKESYHSLPS 220
---PKIGTPTRPCPLPPGNDSPKEKDPEMFCDPFTSATTTTNKEADPSNFANFSAYPS
                                                             APAPKLALRETPAPLPVTSSEP-STTPNNWADFSSTWPSSSNEKPETDNWDTWAAQPS 871
                                                                                                                           SFGGGFADFSTLSKVNNEDPFRSATSSSVSNVVITKNVFEETSVKSEDEPPÄLP-----
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Best Local Similarity
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OTHER INFORMATION: Xaa
-09-764-881-132
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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OTHER INFORMATION:
NAME/KEY: SITE
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ORGANISM:
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                                                                                                                                                               FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                      APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-08-03
                                    APPLICATION NUMBER: PCT/US01/00663
                                                        APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                             FILING DATE:
                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                             FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00666
                     FILING DATE:
APPLICATION NUMBER: PCT/US01/00662
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Chen, Wensheng
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Hanzel, David K.
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Pred. No. 1.4e-15;
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                                           FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: DET/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
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Patent No.
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Best Local Similarity
Matches 79; Conserv
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-29
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o. US20020048763A1
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NX: EXPRESSED IN HELA, SIGNAL = 1.6

NX: EXPRESSED IN HELA, SIGNAL = 2.3

NX: EXPRESSED IN PLACENTA, SIGNAL = 1.6

NX: EXPRESSED IN HT474, SIGNAL = 1.6

NX: EXPRESSED IN HT474, SIGNAL = 1.8

NX: EXPRESSED IN HELACH MARROW, SIGNAL = 1.8

NX: EXPRESSED IN LUNG, SIGNAL = 3.2

NX: EXPRESSED IN LUNG, SIGNAL = 2.7

NX: EXPRESSED IN HELACT, SIGNAL = 2.7

NX: EXPRESSED IN HELACT, SIGNAL = 2.2

NX: EXPRESSED IN HELACT, SIGNAL = 2.7

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Pred. No. 6.6e-16;
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC;
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00668
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b. US20020048763A1
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JN: EXPRESSED IN BYA74,

ON: EXPRESSED IN BONE MARROW, SIGNAL

ION: EXPRESSED IN HBL100, SIGNAL = 1.3

TON: EXPRESSED IN HBL100, SIGNAL = 0.66

TION: EXPRESSED IN LUNG, SIGNAL = 0.66

TION: EXPRESSED IN LUNG, SIGNAL = 0.69

ATION: EXPRESSED IN BRAIN, SIGNAL = 0.92

ATION: EXPRESSED IN HBLA, SIGNAL = 0.92

AATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98

AATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98

TOTH HUMAN HIT: AA773823.1, EVALUE 2.00e-45
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Pred. No. 6.6e-16;
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   GENERAL INFORMATION:
APPLICANT: Penn, Sharron G
                                   Sequence 46565, Application US/09864761 Patent No. US20020048763A1
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TYPE: PRT
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33635
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APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00667
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IN HELA, SIGNAL = 3.7
IN ADULT LIVER, SIGNAL = 3
IN LUNG, SIGNAL = 2.2
HIT: O35601, EVALUE 2.80e-01
HIT: AA815076.1, EVALUE 1.00e-08
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Pred. No. 1.1e-15;
4; Mismatches 2;
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HBL100, SIGNAL = 3.
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: US 09/632,366
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OTHER INFORMATION: MAP TO
OTHER INFORMATION: EXPRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO 46565
ENGTH: 82
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00663
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827 APLPVTSSEPSTTPNNWADFSS 848
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                                                                                                                                                         Similarity
                                                                        VDESQTGEPGWLGGELKGKTGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPKLALRETP
                                         VDESQTGEPGWLGGELKGKTGWFPANYAEKI PENEVPAPVKPVTDSTSAPAPKLALRETP
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                                                                                                                                    Conservative
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N: EXPRESSED IN HELA, SIGNAL = 2.4

N: EXPRESSED IN PLACENTA, SIGNAL = 1.2

N: EXPRESSED IN PLATA, SIGNAL = 0.76

N: EXPRESSED IN HEL100, SIGNAL = 1.3

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95

N: EXPRESSED IN HOME WARROW, SIGNAL = 0.95

N: SWISSPROT HIT: Q15811, EVALUE 9.00e-45

N: EST_HUMAN HIT: AA773823.1, EVALUE 2.00e-37
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Pred. No. 1.4e-15;
0; Mismatches 4
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PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
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SEQ ID NO 34169
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: PCT/US01/00668
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Chen, Wensheng
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Hanzel, David K.
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ED IN BONE MARROW, SIGNAL = 3.3
ED IN ADULT LIVER, SIGNAL = 3.2
ED IN BRAIN, SIGNAL = 4
ED IN BRAIN, SIGNAL = 3.3
ED IN PLACENTA, SIGNAL = 3.3
ED IN HBLIOO, SIGNAL = 2.9
ED IN LUNG, SIGNAL = 3.2
ED IN LUNG, SIGNAL = 3.5
ED IN HELA, SIGNAL = 3.5
ED IN HELA, SIGNAL = 5.3
ED IN HELA, SIGNAL = 2.9
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; LOCATION: (159)
; OTHER INFORMATION: X
; NAME/KEY: SITE
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US-09-764-881-128
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US-09-764-881-128
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Matches 87
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 128
LENGTH: 168
TYPE: PRT
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ07
                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
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LOCATION: (147)
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LOCATION: (77)
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OTHER INFORMATION:
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Local Similarity 96.6%;
nes 84; Conservative
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Local Similarity 60.4%;
98 87; Conservation
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                                                                     IWALADMNNDGRMDQVEFSIAMKLIKLKLQGYQLPSTLPPVMKQQPV--AISSAPAFGIG 118
                                                                                                     MAQFFTAMNGGPNMXAITSEERTKHDRQFDNLKPSGGYITGDQARNFXLQSGLPAPVLAE 67
                                                                                                                            MAQFPTPFGGSLDVWAITVEERAKHDQQFLSLKPIAGFITGDQARNFFFQSGLPQPVLAQ
                                                   IWALSDLNXXGKMDQQEFSIAMKLIKLKLQGQQLPVVLPPIMKQPPMFSPLISA-RFGMG
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o. US20030125246A9
SMPNLSIPOPLPPAA-PITSL 146
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Pred. No. 1.5e-14;
18; Mismatches 32
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Pred. No. 4.5e-15;
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RESULT 15 US-10-171-311-83

Sequence 83, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert

APPLICANT:

Chen, Yan Zhao, Xumei Monahan, John

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APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or
TITLE OF INVENTION: to Genomic Host DNA
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CURRENT APPLICATION NUMBER: US/10/294,804
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/410,399
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.8%; Score 363.5; DB 15; Length 2701; Best Local Similarity 20.7%; Pred. No. 1e-10; Matches 280; Conservative 165; Mismatches 490; Indels 415; Gaps
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Best Local Similarity
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SOFTWARE: FastSEQ for
SEQ ID NO 83
LENGTH: 2701
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APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
    536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 SSFSRSGPGSQLNTKLQKAQSFDVASAPPAAEWAVPQSSRLKYRQLFNSHDKTMSGHLTG
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                                                                                                                                                                    IRCRLATQRQE----IESTNKSRELRIAEITH---------
                                                                                                                                                                                                                                                   RQR----QLEWERNRRQELLNQRNKEQEGTVVLKARRKTLEFELEALNDKKHQLEGKLQD
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEDE-----QQPEKKLPVTFEDKKKENFERGSVELEKRRQALLEQQRKEQERLAQLER 387
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                                       PRFQRQQEQMKQQQWQQQQQQCGVLPQTVPSQPSSSTVPPPPHRPLYQPMQPHPQHLASMG
                                                                                                                            QESENSCNKEEEPVFTRQDSNRS-EKEATPVVHETEPESGSQPRPAVLSGYFKQFQKSLP-672
                                                                                                                                                                                                         PQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEEFILAMHLIDVAMSGQPLPPVLPPE 302
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Glatt, Karen
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                                                                                      --LQQQLQESQQ-----
    ----MLGR---
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-----LIPEKQILSDQLKQVQQNSLH-----
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